

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 14, 2004, 10:28:18 ; Search time 32.5171 Seconds
(without alignments)
165.965 Million cell updates/sec

Title: US-09-843-221A-162
Perfect score: 34
Sequence: 1 SVSEIQLMHNRGKHLNSMERVEWLRKKLQDVHNF 34

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 75810

Minimum DB seq length: 28
Maximum DB seq length: 40

Post-processing: Listing first 1000 summaries

Database : A_Geneseq_19Jun03:*

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- 23: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
- 24: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	34	100.0	34	23	AAU73029	Parathyroid hormon
2	34	100.0	35	23	AAU73173	Parathyroid hormon
3	30	88.2	30	23	AAU73052	Parathyroid hormon
4	23	67.6	28	13	AAR22064	Modified hPTH(7-34
5	23	67.6	28	21	ABJ10776	Human parathyroid
6	23	67.6	28	23	AAE23734	Human parathyroid
7	23	67.6	28	23	AAU73044	Parathyroid hormon
8	23	67.6	30	23	AAE23752	Human parathyroid
9	23	67.6	32	21	AAB07468	Antigenic peptide
10	23	67.6	32	23	AAE23735	Human parathyroid
11	23	67.6	34	4	AAP30022	Human parathyroid-
12	23	67.6	34	6	AAP50377	[Met(O)8,18]hPTH-(
13	23	67.6	34	7	AAP60031	Sequence of the fi
14	23	67.6	34	11	AAR07919	Human parathyroid
15	23	67.6	34	13	AAR22283	Parathyroid hormon
16	23	67.6	34	13	AAR22292	Human parathyroid
17	23	67.6	34	13	AAR22293	Human parathyroid
18	23	67.6	34	13	AAR22294	Human parathyroid
19	23	67.6	34	13	AAR22296	Human parathyroid
20	23	67.6	34	14	AAR41549	[D-Ser3]hPTH (1-34
21	23	67.6	34	14	AAR41550	[D-Ala3]hPTH (1-34
22	23	67.6	34	14	AAR41570	[Gln25]hPTH (1-34)
23	23	67.6	34	15	AAR49697	Sequence of varian
24	23	67.6	34	15	AAR49698	Sequence of varian
25	23	67.6	34	15	AAR58291	[Lys(For)26, Lys(F
26	23	67.6	34	15	AAR58228	[D-Asp30]-hPTH(1-3
27	23	67.6	34	15	AAR58016	N-alpha-Isopropyl-
28	23	67.6	34	15	AAR58017	[Lys(N-epsilon-Iso
29	23	67.6	34	15	AAR55724	Parathormone N-ter
30	23	67.6	34	16	AAR74521	Human parathyroid
31	23	67.6	34	17	AAW99449	Human parathyroid
32	23	67.6	34	17	AAW15812	[Trp(10)]-hPTH(1-3
33	23	67.6	34	17	AAR99978	Human parathyroid
34	23	67.6	34	17	AAR98951	Target peptide (PT
35	23	67.6	34	17	AAR98966	PTH(1-34).. Not sp
36	23	67.6	34	17	AAR88835	Human parathyroid
37	23	67.6	34	18	AAW24273	Wild type parathyr
38	23	67.6	34	18	AAW08120	Human PTH derivati
39	23	67.6	34	18	AAW08108	Human parathyroid
40	23	67.6	34	18	AAW08109	Human parathyroid
41	23	67.6	34	18	AAW08113	Human PTH derivati
42	23	67.6	34	18	AAW08114	Human PTH derivati
43	23	67.6	34	18	AAW08117	Human PTH derivati
44	23	67.6	34	18	AAW08118	Human PTH derivati
45	23	67.6	34	18	AAW08119	Human PTH derivati
46	23	67.6	34	18	AAW19994	Cyclised human par
47	23	67.6	34	18	AAW20000	Cyclised human par
48	23	67.6	34	18	AAW20006	Cyclised human par
49	23	67.6	34	18	AAW17941	Human parathyroid
50	23	67.6	34	18	AAW17943	Human parathyroid

51	23	67.6	34	18	AAW17939	Human parathyroid
52	23	67.6	34	18	AAW17957	Human parathyroid
53	23	67.6	34	18	AAW01609	Parathyroid hormon
54	23	67.6	34	19	AAW67274	Parathyroid hormon
55	23	67.6	34	19	AAW67276	Parathyroid hormon
56	23	67.6	34	19	AAW67278	Parathyroid hormon
57	23	67.6	34	19	AAW67290	Parathyroid hormon
58	23	67.6	34	19	AAW67291	Parathyroid hormon
59	23	67.6	34	19	AAW67299	Parathyroid hormon
60	23	67.6	34	19	AAW61658	Parathyroid hormon
61	23	67.6	34	19	AAW65975	Human parathyroid
62	23	67.6	34	20	AAV50593	Resin bound cyclic
63	23	67.6	34	20	AAV17752	Human parathyroid
64	23	67.6	34	20	AAV14151	Human parathyroid
65	23	67.6	34	20	AAV02579	N-terminal 34 resi
66	23	67.6	34	20	AAW81871	Human PTH N-termin
67	23	67.6	34	21	ABJ10706	Human parathyroid
68	23	67.6	34	21	ABJ10712	Human parathyroid
69	23	67.6	34	21	ABJ10713	Human parathyroid
70	23	67.6	34	21	ABJ10714	Human parathyroid
71	23	67.6	34	21	ABJ10717	Human parathyroid
72	23	67.6	34	21	ABJ10719	Human parathyroid
73	23	67.6	34	21	ABJ10722	Human parathyroid
74	23	67.6	34	21	ABJ10724	Human parathyroid
75	23	67.6	34	21	ABJ10727	Human parathyroid
76	23	67.6	34	21	ABJ10729	Human parathyroid
77	23	67.6	34	21	ABJ10730	Human parathyroid
78	23	67.6	34	21	ABJ10733	Human parathyroid
79	23	67.6	34	21	ABJ10736	Human parathyroid
80	23	67.6	34	21	ABJ10737	Human parathyroid
81	23	67.6	34	21	ABJ10769	Human parathyroid
82	23	67.6	34	21	AAB07454	Amino acids 1-34 o
83	23	67.6	34	21	AAV98010	Human amino-termin
84	23	67.6	34	21	AAV98011	Human amino-termin
85	23	67.6	34	21	AAV98014	Human amino-termin
86	23	67.6	34	21	AAV98017	Human amino-termin
87	23	67.6	34	21	AAV82631	Human parathyroid
88	23	67.6	34	21	AAV68763	Amino acids 1-34 o
89	23	67.6	34	22	AAB84778	Native rat parathy
90	23	67.6	34	22	AAB96898	Human parathyroid
91	23	67.6	34	22	AAB81079	Human parathyroid
92	23	67.6	34	22	AAB91098	Parathyroid hormon
93	23	67.6	34	22	AAB91113	Parathyroid hormon
94	23	67.6	34	22	AAB61638	Peptide #1 that ca
95	23	67.6	34	23	ABJ05328	Human PTH(1-34) pe
96	23	67.6	34	23	AAE23727	Human parathyroid
97	23	67.6	34	23	AAE23728	Human parathyroid
98	23	67.6	34	23	ABB06329	Human parathyroid
99	23	67.6	34	23	ABB08595	C-terminal truncat
100	23	67.6	34	23	AAE18395	Human PTH peptide
101	23	67.6	34	23	AAE18399	Human PTH peptide
102	23	67.6	34	23	ABB07147	Parathyroid hormon
103	23	67.6	34	23	AAU73028	Parathyroid hormon
104	23	67.6	34	23	AAU73030	Parathyroid hormon
105	23	67.6	34	23	AAU73032	Parathyroid hormon
106	23	67.6	34	24	ABP71500	Human parathyroid
107	23	67.6	34	24	ABG74235	Human parathyroid

108	23	67.6	35	22	AAB91112	Parathyroid hormon
109	23	67.6	35	23	AAU73172	Parathyroid hormon
110	23	67.6	36	12	AAR15842	Human parathyroid
111	23	67.6	36	13	AAR23995	Human paprthyroid
112	23	67.6	36	14	AAR39450	Ser-Val-(hPTH 3-35
113	23	67.6	36	15	AAR58286	[D-Leu24]-hPTH(1-3
114	23	67.6	36	15	AAR58292	[D-Lys27]-hPTH(1-3
115	23	67.6	36	15	AAR58293	[D-Leu28]-hPTH(1-3
116	23	67.6	36	15	AAR58294	[D-Phe34]-hPTH(1-3
117	23	67.6	36	15	AAR58295	[D-Val35]-hPTH(1-3
118	23	67.6	36	15	AAR58296	[Ala35]-hPTH(1-36)
119	23	67.6	36	15	AAR58297	[Pro35]-hPTH(1-36)
120	23	67.6	36	15	AAR58298	[NMeVal35]-hPTH(1-
121	23	67.6	36	15	AAR58299	[Thr35,Ala36]-hPTH
122	23	67.6	36	15	AAR58300	[D-Ala36]-hPTH(1-3
123	23	67.6	36	15	AAR58301	[NMeAla36]-hPTH(1-
124	23	67.6	36	15	AAR58254	[4-aminosalicylic
125	23	67.6	36	15	AAR58255	[TMSA1]-hPTH(1-36)
126	23	67.6	36	15	AAR58256	[Phe1]-hPTH(1-36)-
127	23	67.6	36	15	AAR58257	[Propargylglycin1]
128	23	67.6	36	15	AAR58259	[aBU2]-hPTH(1-36)-
129	23	67.6	36	15	AAR58260	[D-Val2]-hPTH(1-36
130	23	67.6	36	15	AAR58261	[Tert.Leu]-hPTH(1-
131	23	67.6	36	15	AAR58262	[Ala1]-hPTH(1-36)-
132	23	67.6	36	15	AAR58263	[D-Ile5]-hPTH(1-36
133	23	67.6	36	15	AAR58264	[D-Gln6]-hPTH(1-36
134	23	67.6	36	15	AAR58265	[D-Leu7]-hPTH(1-36
135	23	67.6	36	15	AAR58266	[Nle8]-hPTH(1-36)-
136	23	67.6	36	15	AAR58267	[Phe8]-hPTH(1-36)-
137	23	67.6	36	15	AAR58268	[Cha8]-hPTH(1-36)-
138	23	67.6	36	15	AAR58270	[D-Leu11]-hPTH(1-3
139	23	67.6	36	15	AAR58271	[Ala11]-hPTH(1-36)
140	23	67.6	36	15	AAR58272	[D-Lys13]-hPTH(1-3
141	23	67.6	36	15	AAR58273	[D-Leu15]-hPTH(1-3
142	23	67.6	36	15	AAR58276	[Met(O2)18]-hPTH(1
143	23	67.6	36	15	AAR58278	[D-Met18]-hPTH(1-3
144	23	67.6	36	15	AAR58280	[D-Arg20]-hPTH(1-3
145	23	67.6	36	15	AAR58281	[D-Val21]-hPTH(1-3
146	23	67.6	36	15	AAR58284	[D-Trp23]-hPTH(1-3
147	23	67.6	36	15	AAR58227	[D-Gln29]-hPTH(1-3
148	23	67.6	36	15	AAR58230	[D-Val31]-hPTH(1-3
149	23	67.6	36	15	AAR58233	[D-His32]-hPTH(1-3
150	23	67.6	36	15	AAR58235	[D-Asn33]-hPTH(1-3
151	23	67.6	36	15	AAR58237	[NMePhe34]-hPTH(1-
152	23	67.6	36	15	AAR58238	[D-Asp30]-hPTH(1-3
153	23	67.6	36	15	AAR58242	[Lys(Isopropyl)13]
154	23	67.6	36	15	AAR58243	Propargyl-[A1]-hPT
155	23	67.6	36	15	AAR58246	Acetyl-hPTH(1-36)-
156	23	67.6	36	15	AAR58247	[Hyp1]-hPTH(1-36)-
157	23	67.6	36	15	AAR58248	N-Dimethyl-[Ala1]-
158	23	67.6	36	15	AAR58249	[D-Ser1]-hPTH(1-36
159	23	67.6	36	15	AAR58250	[Lys(For)1]-hPTH(1
160	23	67.6	36	15	AAR58251	[D-glyceric acid1]
161	23	67.6	36	15	AAR58252	[Asn1]-hPTH(1-36)-
162	23	67.6	36	15	AAR58253	[4-aminobenzoic ac
163	23	67.6	36	15	AAR58196	[D-Phe34, D-Ala36]
164	23	67.6	36	15	AAR58197	[Ala3]-hPTH(1-36)-

165	23	67.6	36	15	AAR58198	[D-Ser3]-hPTH(1-36
166	23	67.6	36	15	AAR58199	[D-Glu4]-hPTH(1-36
167	23	67.6	36	15	AAR58200	[D-His9]-hPTH(1-36
168	23	67.6	36	15	AAR58201	[Ala10]-hPTH(1-36)
169	23	67.6	36	15	AAR58202	[D-Asn10]-hPTH(1-3
170	23	67.6	36	15	AAR58210	[D-His14]-hPTH(1-3
171	23	67.6	36	15	AAR58211	[D-Asn16]-hPTH(1-3
172	23	67.6	36	15	AAR58213	[D-Ser17]-hPTH(1-3
173	23	67.6	36	15	AAR58215	[D-Glu19]-hPTH(1-3
174	23	67.6	36	15	AAR58220	[D-Lys26]-hPTH(1-3
175	23	67.6	36	15	AAR58169	[D-Prol]-hPTH(1-36
176	23	67.6	36	15	AAR58170	[Nva1]-hPTH(1-36)-
177	23	67.6	36	15	AAR58171	[N-Me-Ser1]-hPTH(1
178	23	67.6	36	15	AAR58172	[Indole-2-carboxyl
179	23	67.6	36	15	AAR58173	[Indole-3-carboxyl
180	23	67.6	36	15	AAR58174	[Pyridine-3-carbox
181	23	67.6	36	15	AAR58175	[Pyridine-2-carbox
182	23	67.6	36	15	AAR58176	[Hexahydropyridazi
183	23	67.6	36	15	AAR58177	[Morpholine-2-carb
184	23	67.6	36	15	AAR58178	[Pro1]-hPTH(1-36)-
185	23	67.6	36	15	AAR58179	[Leu1]-hPTH(1-36)-
186	23	67.6	36	15	AAR58180	[Ile1]-hPTH(1-36)-
187	23	67.6	36	15	AAR58182	[Nva8]-hPTH(1-36)-
188	23	67.6	36	15	AAR58026	N-alpha-methyl [Ala
189	23	67.6	36	15	AAR58168	[1-amino-cyclopent
190	23	67.6	37	12	AAR11882	Parathyroid hormon
191	23	67.6	37	13	AAR24778	hPTH(1-37)-amide/e
192	23	67.6	37	15	AAR58244	[Ala0]-hPTH(1-36)-
193	23	67.6	37	15	AAR58245	[Pro0]-hPTH(1-36)-
194	23	67.6	37	22	AAB86226	Human parathyroid
195	23	67.6	37	22	AAB86229	Human parathyroid
196	23	67.6	37	23	ABB82203	Human parathyroid
197	23	67.6	37	23	AAU73027	Parathyroid hormon
198	23	67.6	38	15	AAR58269	[Leu8]-hPTH(1-38)-
199	23	67.6	38	15	AAR58282	[Trp(SO2Pmc)23]-hP
200	23	67.6	38	15	AAR58283	[Trp(Pmc)23]-hPTH(
201	23	67.6	38	15	AAR58018	Isopropyl-[Lys(Iso
202	23	67.6	38	15	AAR58019	N-alpha-methyl [Ala
203	23	67.6	38	15	AAR58022	[Ile1]-hPTH(1-38)-
204	23	67.6	38	15	AAR58023	[Ala1, Abu2 or Nva2
205	23	67.6	38	15	AAR58024	[Ala1, Ile2]-hPTH(1
206	23	67.6	38	15	AAR58028	[Thr1]-hPTH(1-38)-
207	23	67.6	38	15	AAR58029	[Leu1]-hPTH(1-38)-
208	23	67.6	38	15	AAR58030	[Abu1 or Gabal]-hP
209	23	67.6	38	15	AAR54234	PTH N-terminal. S
210	23	67.6	38	17	AAR98958	Target peptide (PT
211	23	67.6	38	20	AAY02580	N-terminal 38 resi
212	23	67.6	38	22	AAB91101	Parathyroid hormon
213	23	67.6	38	23	AAE23729	Human parathyroid
214	23	67.6	38	23	AAE18400	Human PTH peptide
215	23	67.6	38	23	AAU73026	Parathyroid hormon
216	22	64.7	28	13	AAR22065	Modified [Tyr_34]h
217	22	64.7	31	5	AAP40760	Human parathyroid
218	22	64.7	32	5	AAP40427	Parathyroid antago
219	22	64.7	33	17	AAR88841	Human parathyroid
220	22	64.7	33	21	AAY98012	Human amino-termin
221	22	64.7	33	21	AAY98015	Human amino-termin

222	22	64.7	33	21	AAAY98018	Human amino-termin
223	22	64.7	34	11	AAR07922	Human parathyroid
224	22	64.7	34	11	AAR08300	Human parathyroid
225	22	64.7	34	18	AAW08121	Human PTH derivati
226	22	64.7	34	18	AAW08115	Human PTH derivati
227	22	64.7	34	18	AAW08116	Human PTH derivati
228	22	64.7	34	18	AAW17955	Human parathyroid
229	22	64.7	34	18	AAW17959	Human parathyroid
230	22	64.7	34	19	AAW48392	Human parathyroid
231	22	64.7	34	21	ABJ10772	Human parathyroid
232	22	64.7	34	21	ABJ10773	Human parathyroid
233	22	64.7	34	22	AAB96929	Human parathyroid
234	22	64.7	36	15	AAR58191	[Ala34]-hPTH(1-36)
235	22	64.7	36	15	AAR58203	[Ala12]-hPTH(1-36)
236	22	64.7	38	3	AAP20248	Parathyroid hormon
237	22	64.7	38	15	AAR58089	[Arg12]-hPTH(1-38)
238	22	64.7	38	15	AAR58090	[Ser12]-hPTH(1-38)
239	21	61.8	28	13	AAR22066	Modified [D-Trp ₁₂
240	21	61.8	32	17	AAR88840	Human parathyroid
241	21	61.8	34	11	AAR08303	Human parathyroid
242	21	61.8	34	15	AAR58193	[L8,D10,K11,T33,A3
243	21	61.8	34	15	AAR58194	[A1,H5,L8,D10,K11,
244	21	61.8	34	15	AAR58181	[Thr33, Ala34]-hPT
245	21	61.8	34	18	AAW08112	Human PTH derivati
246	21	61.8	34	19	AAW42614	Human parathyroid
247	21	61.8	34	22	AAB96893	Rat parathyroid ho
248	21	61.8	34	22	AAB96930	Rat parathyroid ho
249	21	61.8	36	15	AAR58236	[Ala33]-hPTH(1-36)
250	21	61.8	36	15	AAR58204	[Gln13]-hPTH(1-36)
251	21	61.8	36	15	AAR58205	[His13]-hPTH(1-36)
252	21	61.8	36	15	AAR58206	[Leu13]-hPTH(1-36)
253	21	61.8	36	15	AAR58207	[Ala13]-hPTH(1-36)
254	21	61.8	38	15	AAR58161	[Pro3,Thr33]-hPTH(
255	21	61.8	38	15	AAR58162	[Arg33]-hPTH(1-38)
256	21	61.8	38	15	AAR58163	[Pro33]-hPTH(1-38)
257	21	61.8	38	15	AAR58164	[Asp33]-hPTH(1-38)
258	21	61.8	38	15	AAR58165	[Ile33]-hPTH(1-38)
259	21	61.8	38	15	AAR58166	[Lys33]-hPTH(1-38)
260	21	61.8	38	15	AAR58075	[Ser33]-hPTH(1-38)
261	21	61.8	38	15	AAR58076	[Thr33]-hPTH(1-38)
262	21	61.8	38	15	AAR58077	[Leu33]-hPTH(1-38)
263	21	61.8	38	15	AAR58078	[Gly33]-hPTH(1-38)
264	21	61.8	38	15	AAR58084	[Gln33]-hPTH(1-38)
265	21	61.8	38	15	AAR58091	[Cys13]-hPTH(1-38)
266	21	61.8	38	15	AAR58092	[Ile13]-hPTH(1-38)
267	21	61.8	38	15	AAR58093	[Asn13]-hPTH(1-38)
268	21	61.8	38	15	AAR58094	[Trp13]-hPTH(1-38)
269	21	61.8	38	15	AAR58095	[Asp13]-hPTH(1-38)
270	21	61.8	38	15	AAR58096	[Val13]-hPTH(1-38)
271	21	61.8	38	15	AAR58097	[Thr13]-hPTH(1-38)
272	21	61.8	38	15	AAR58098	[Ser13]-hPTH(1-38)
273	21	61.8	38	15	AAR58099	[Tyr13]-hPTH(1-38)
274	21	61.8	38	15	AAR58100	[Met13]-hPTH(1-38)
275	21	61.8	38	15	AAR58101	[Gln13]-hPTH(1-38)
276	21	61.8	38	15	AAR58102	[Leu13]-hPTH(1-38)
277	21	61.8	38	15	AAR58103	[Ala13]-hPTH(1-38)
278	21	61.8	38	15	AAR58104	[Gly13]-hPTH(1-38)

279	20	58.8	30	6	AAP50665	Human parathyroid
280	20	58.8	31	17	AAR88830	Human parathyroid
281	20	58.8	31	19	AAW42059	Human parathyroid
282	20	58.8	31	19	AAW42051	Human parathyroid
283	20	58.8	31	20	AAV02578	N-terminal 31 resi
284	20	58.8	31	22	AAB81080	Human parathyroid
285	20	58.8	31	22	AAB91097	Parathyroid hormon
286	20	58.8	31	23	AAE23720	Human parathyroid
287	20	58.8	31	23	AAU73039	Parathyroid hormon
288	20	58.8	32	23	AAU73176	Parathyroid hormon
289	20	58.8	34	15	AAR58232	[Lys32]-hPTH(1-34)
290	20	58.8	34	18	AAW08129	Human PTH derivati
291	20	58.8	34	22	AAB84771	Parathyroid hormon
292	20	58.8	34	22	AAB84826	Parathyroid hormon
293	20	58.8	34	22	AAB96916	Parathyroid hormon
294	20	58.8	34	22	AAB96919	Parathyroid hormon
295	20	58.8	36	15	AAR58234	[Ala32]-hPTH(1-36)
296	20	58.8	36	15	AAR58209	[Ala14]-hPTH(1-36)
297	20	58.8	38	15	AAR58037	[Ser14]-hPTH(1-38)
298	20	58.8	38	15	AAR58105	[Val14]-hPTH(1-38)
299	20	58.8	38	15	AAR58106	[Ala14]-hPTH(1-38)
300	20	58.8	38	15	AAR58107	[Lys14]-hPTH(1-38)
301	20	58.8	38	15	AAR58108	[Arg14]-hPTH(1-38)
302	20	58.8	38	15	AAR58109	[Thr14]-hPTH(1-38)
303	20	58.8	38	15	AAR58110	[Ile14]-hPTH(1-38)
304	20	58.8	38	15	AAR58111	[Tyr14]-hPTH(1-38)
305	19	55.9	30	17	AAR88832	Human parathyroid
306	19	55.9	30	23	AAU73051	Parathyroid hormon
307	19	55.9	30	23	AAU73053	Parathyroid hormon
308	19	55.9	30	23	AAU73055	Parathyroid hormon
309	19	55.9	31	23	AAU73177	Parathyroid hormon
310	19	55.9	34	18	AAW17942	Human parathyroid
311	19	55.9	34	18	AAW17948	Human parathyroid
312	19	55.9	34	18	AAW17968	Human parathyroid
313	19	55.9	34	18	AAW17952	Human parathyroid
314	19	55.9	34	19	AAW67277	Parathyroid hormon
315	19	55.9	34	19	AAW67283	Parathyroid hormon
316	19	55.9	34	19	AAW67287	Parathyroid hormon
317	19	55.9	34	19	AAW48394	Human PTH/PTHrP hy
318	19	55.9	35	23	AAU73174	Parathyroid hormon
319	19	55.9	36	15	AAR58274	[Ala15]-hPTH(1-36)
320	19	55.9	36	15	AAR58231	[Ala31]-hPTH(1-36)
321	19	55.9	38	15	AAR58061	[Ile15]-hPTH(1-38)
322	19	55.9	38	15	AAR58167	[Ile31,Arg33]-hPTH
323	19	55.9	38	15	AAR58112	[Tyr15]-hPTH(1-38)
324	19	55.9	38	15	AAR58113	[Arg15]-hPTH(1-38)
325	19	55.9	38	15	AAR58114	[Val15]-hPTH(1-38)
326	18	52.9	28	13	AAR22058	Modified bovine PT
327	18	52.9	28	23	AAU73046	Parathyroid hormon
328	18	52.9	29	17	AAR88836	Human parathyroid
329	18	52.9	29	23	AAU73063	Parathyroid hormon
330	18	52.9	30	23	AAU73178	Parathyroid hormon
331	18	52.9	32	22	AAB91096	Parathyroid hormon
332	18	52.9	32	23	AAE23739	Bovine parathyroid
333	18	52.9	32	23	AAE18402	Bovine PTH peptide
334	18	52.9	32	23	AAU73042	Parathyroid hormon
335	18	52.9	34	11	AAR07918	Bovine parathyroid

336	18	52.9	34	11	AAR08299	Bovine parathyroid
337	18	52.9	34	14	AAR41551	[Thr16]hPTH (1-34)
338	18	52.9	34	14	AAR41552	[Glu16]hPTH (1-34)
339	18	52.9	34	14	AAR41553	[Lys16]hPTH (1-34)
340	18	52.9	34	14	AAR41571	[D-Lys16]hPTH (1-34)
341	18	52.9	34	14	AAR41573	[Gln16]hPTH (1-34)
342	18	52.9	34	14	AAR41574	[Ser16]hPTH (1-34)
343	18	52.9	34	14	AAR41575	[Gly16]hPTH (1-34)
344	18	52.9	34	14	AAR41576	[Lys16]hPTH (1-34)
345	18	52.9	34	17	AAR99979	Bovine parathyroid
346	18	52.9	34	18	AAW08124	Human PTH derivati
347	18	52.9	34	18	AAW08111	Human PTH derivati
348	18	52.9	34	18	AAW19995	Cyclised bovine pa
349	18	52.9	34	18	AAW20001	Cyclised bovine pa
350	18	52.9	34	18	AAW20007	Cyclised bovine pa
351	18	52.9	34	18	AAW17953	Human parathyroid
352	18	52.9	34	18	AAW17963	Human PTH analogue
353	18	52.9	34	19	AAW61659	Parathyroid hormon
354	18	52.9	34	19	AAW65976	Bovine parathyroid
355	18	52.9	34	19	AAW42615	Bovine parathyroid
356	18	52.9	34	20	AAW81872	Bovine PTH N-termi
357	18	52.9	34	22	AAB84775	Parathyroid hormon
358	18	52.9	34	22	AAB96922	Parathyroid hormon
359	18	52.9	34	23	AAE23738	Bovine parathyroid
360	18	52.9	34	23	AAE18394	Bovine PTH peptide
361	18	52.9	34	23	AAU73034	Parathyroid hormon
362	18	52.9	36	15	AAR58275	[Ala16]-hPTH(1-36)
363	18	52.9	36	15	AAR58229	[Ala30]-hPTH(1-36)
364	18	52.9	37	22	AAB86230	Bovine parathyroid
365	18	52.9	37	22	AAB86233	Canine parathyroid
366	18	52.9	37	23	ABB82204	Bovine parathyroid
367	18	52.9	38	15	AAR58036	[Gln16]-hPTH(1-38)
368	18	52.9	38	15	AAR58115	[Lys16]-hPTH(1-38)
369	18	52.9	38	15	AAR58116	[Ser16]-hPTH(1-38)
370	18	52.9	38	15	AAR58117	[Leu16]-hPTH(1-38)
371	18	52.9	38	15	AAR58118	[Ala16]-hPTH(1-38)
372	18	52.9	38	15	AAR58119	[Gly16]-hPTH(1-38)
373	17	50.0	28	13	AAR22059	Modified [Tyr_34]b
374	17	50.0	28	13	AAR22060	Modified [D-Trp_12
375	17	50.0	28	17	AAR88837	Human parathyroid
376	17	50.0	28	21	AAV98048	Human parathyroid
377	17	50.0	28	21	AAV98050	Human parathyroid
378	17	50.0	28	21	AAV98052	Human parathyroid
379	17	50.0	28	22	AAB91115	Parathyroid hormon
380	17	50.0	28	23	AAE18405	Bovine PTH peptide
381	17	50.0	28	23	AAU73047	Parathyroid hormon
382	17	50.0	28	23	AAU73050	Parathyroid hormon
383	17	50.0	28	23	AAU73064	Parathyroid hormon
384	17	50.0	29	12	AAR11731	Adenine-rich PTH-(
385	17	50.0	29	23	AAU73179	Parathyroid hormon
386	17	50.0	31	5	AAP40510	Bovine parathyroid
387	17	50.0	31	21	AAV96973	Parathyroid hormon
388	17	50.0	31	21	AAV96974	Parathyroid hormon
389	17	50.0	34	11	AAR07921	Bovine parathyroid
390	17	50.0	34	11	AAR08302	Bovine parathyroid
391	17	50.0	34	14	AAR41577	[Lys16, Asp17]hPTH
392	17	50.0	34	14	AAR41578	[Lys14,15,16,17]hP

393	17	50.0	34	14	AAR41579	[Lys15,15,17]hPTH
394	17	50.0	34	14	AAR41580	[Lys16,17]hPTH (1-
395	17	50.0	34	14	AAR41581	[Arg16,17]hPTH (1-
396	17	50.0	34	14	AAR41582	[Arg15,16,17]hPTH
397	17	50.0	34	17	AAW14308	Cyclic parathyroid
398	17	50.0	34	17	AAW14309	Cyclic parathyroid
399	17	50.0	34	17	AAW14310	Cyclic parathyroid
400	17	50.0	34	17	AAW14311	Cyclic parathyroid
401	17	50.0	34	17	AAW14312	Cyclic parathyroid
402	17	50.0	34	17	AAW14313	Cyclic parathyroid
403	17	50.0	34	17	AAW14314	Cyclic parathyroid
404	17	50.0	34	17	AAW14315	Cyclic parathyroid
405	17	50.0	34	18	AAW08122	Human PTH derivati
406	17	50.0	34	18	AAW08123	Human PTH derivati
407	17	50.0	34	18	AAW17958	Human parathyroid
408	17	50.0	34	18	AAW01610	Parathyroid hormon
409	17	50.0	34	19	AAW67293	Parathyroid hormon
410	17	50.0	36	15	AAR58190	[Ala29]-hPTH(1-36)
411	17	50.0	36	15	AAR58212	[Ala17]-hPTH(1-36)
412	17	50.0	38	15	AAR58120	[Ala17]-hPTH(1-38)
413	17	50.0	38	15	AAR58121	[Met17]-hPTH(1-38)
414	17	50.0	38	15	AAR58122	[Ile17]-hPTH(1-38)
415	16	47.1	28	21	ABJ10775	Human parathyroid
416	16	47.1	34	13	AAR22291	Human parathyroid
417	16	47.1	34	13	AAR22295	Human parathyroid
418	16	47.1	34	15	AAR58239	Isopropyl-[Nle8,18
419	16	47.1	34	15	AAR58241	[Nle8,18,D-Asn33,D
420	16	47.1	34	17	AAW14316	Cyclic parathyroid
421	16	47.1	34	17	AAR99981	Porcine parathyroi
422	16	47.1	34	18	AAW17947	Human parathyroid
423	16	47.1	34	18	AAW17951	Human parathyroid
424	16	47.1	34	19	AAW67282	Parathyroid hormon
425	16	47.1	34	19	AAW67286	Parathyroid hormon
426	16	47.1	34	19	AAW67298	Parathyroid hormon
427	16	47.1	34	19	AAW61660	Parathyroid hormon
428	16	47.1	34	19	AAW65977	Porcine parathyroi
429	16	47.1	34	19	AAW42616	Porcine parathyroi
430	16	47.1	34	20	AAW92218	Analogue of parath
431	16	47.1	34	20	AAW92219	Analogue of parath
432	16	47.1	34	20	AAW03920	Analogue of parath
433	16	47.1	34	20	AAW03921	Analogue of parath
434	16	47.1	34	20	AAW03922	Analogue of parath
435	16	47.1	34	20	AAW03923	Analogue of parath
436	16	47.1	34	20	AAW03924	Analogue of parath
437	16	47.1	34	20	AAW03925	Analogue of parath
438	16	47.1	34	20	AAW03926	Analogue of parath
439	16	47.1	34	20	AAW03927	Analogue of parath
440	16	47.1	34	20	AAW03928	Analogue of parath
441	16	47.1	34	20	AAW03929	Analogue of parath
442	16	47.1	34	20	AAW03930	Analogue of parath
443	16	47.1	34	20	AAW03931	Analogue of parath
444	16	47.1	34	20	AAW03932	Analogue of parath
445	16	47.1	34	20	AAW03933	Analogue of parath
446	16	47.1	34	20	AAW92236	Analogue of parath
447	16	47.1	34	20	AAW92237	Analogue of parath
448	16	47.1	34	20	AAW92238	Analogue of parath
449	16	47.1	34	20	AAW92239	Analogue of parath

450	16	47.1	34	20	AAW92240	Analogue of parath
451	16	47.1	34	20	AAW92241	Analogue of parath
452	16	47.1	34	20	AAW92242	Analogue of parath
453	16	47.1	34	20	AAW92243	Analogue of parath
454	16	47.1	34	20	AAW92244	Analogue of parath
455	16	47.1	34	20	AAW92245	Analogue of parath
456	16	47.1	34	20	AAW92246	Analogue of parath
457	16	47.1	34	20	AAW92247	Analogue of parath
458	16	47.1	34	20	AAW92248	Analogue of parath
459	16	47.1	34	20	AAW92249	Analogue of parath
460	16	47.1	34	20	AAW92250	Analogue of parath
461	16	47.1	34	20	AAW92251	Analogue of parath
462	16	47.1	34	20	AAW92220	Analogue of parath
463	16	47.1	34	20	AAW92221	Analogue of parath
464	16	47.1	34	20	AAW92222	Analogue of parath
465	16	47.1	34	20	AAW92223	Analogue of parath
466	16	47.1	34	20	AAW92224	Analogue of parath
467	16	47.1	34	20	AAW92225	Analogue of parath
468	16	47.1	34	20	AAW92226	Analogue of parath
469	16	47.1	34	20	AAW92227	Analogue of parath
470	16	47.1	34	20	AAW92228	Analogue of parath
471	16	47.1	34	20	AAW92229	Analogue of parath
472	16	47.1	34	20	AAW92230	Analogue of parath
473	16	47.1	34	20	AAW92231	Analogue of parath
474	16	47.1	34	20	AAW92232	Analogue of parath
475	16	47.1	34	20	AAW92233	Analogue of parath
476	16	47.1	34	20	AAW92234	Analogue of parath
477	16	47.1	34	20	AAW92235	Analogue of parath
478	16	47.1	34	20	AAW92236	Analogue of parath
479	16	47.1	34	20	AAW92237	Analogue of parath
480	16	47.1	34	20	AAW92204	Analogue of parath
481	16	47.1	34	20	AAW92205	Analogue of parath
482	16	47.1	34	20	AAW92207	Analogue of parath
483	16	47.1	34	20	AAW92208	Analogue of parath
484	16	47.1	34	20	AAW92209	Analogue of parath
485	16	47.1	34	20	AAW92210	Analogue of parath
486	16	47.1	34	20	AAW92211	Analogue of parath
487	16	47.1	34	20	AAW92212	Analogue of parath
488	16	47.1	34	20	AAW92213	Analogue of parath
489	16	47.1	34	20	AAW92214	Analogue of parath
490	16	47.1	34	20	AAW92215	Analogue of parath
491	16	47.1	34	20	AAW92216	Analogue of parath
492	16	47.1	34	20	AAW92217	Analogue of parath
493	16	47.1	34	20	AAW92206	Analogue of parath
494	16	47.1	34	20	AAW92203	Analogue of parath
495	16	47.1	34	20	AAW92204	Analogue of parath
496	16	47.1	34	20	AAW92205	Analogue of parath
497	16	47.1	34	20	AAW92206	Analogue of parath
498	16	47.1	34	20	AAW92207	Analogue of parath
499	16	47.1	34	20	AAW92208	Analogue of parath
500	16	47.1	34	20	AAW92209	Analogue of parath
501	16	47.1	34	20	AAW92210	Analogue of parath
502	16	47.1	34	20	AAW92211	Analogue of parath
503	16	47.1	34	20	AAW92212	Analogue of parath
504	16	47.1	34	20	AAW92213	Analogue of parath
505	16	47.1	34	20	AAW92214	Analogue of parath
506	16	47.1	34	20	AAW92215	Analogue of parath

507	16	47.1	34	20	AAAY03946	Analogue of parath
508	16	47.1	34	20	AAAY03949	Analogue of parath
509	16	47.1	34	20	AAAY03950	Analogue of parath
510	16	47.1	34	20	AAAY03951	Analogue of parath
511	16	47.1	34	20	AAAY03952	Analogue of parath
512	16	47.1	34	20	AAAY03953	Analogue of parath
513	16	47.1	34	20	AAAY03954	Analogue of parath
514	16	47.1	34	20	AAAY03955	Analogue of parath
515	16	47.1	34	20	AAAY03956	Analogue of parath
516	16	47.1	34	20	AAW92198	Analogue of parath
517	16	47.1	34	20	AAW92199	Analogue of parath
518	16	47.1	34	20	AAW92200	Analogue of parath
519	16	47.1	34	20	AAW92201	Analogue of parath
520	16	47.1	34	20	AAW92202	Analogue of parath
521	16	47.1	34	20	AAW92183	Analogue of parath
522	16	47.1	34	20	AAW92184	Analogue of parath
523	16	47.1	34	20	AAW92185	Analogue of parath
524	16	47.1	34	20	AAW92186	Analogue of parath
525	16	47.1	34	20	AAW92187	Analogue of parath
526	16	47.1	34	20	AAW92167	Analogue of parath
527	16	47.1	34	20	AAW92188	Analogue of parath
528	16	47.1	34	20	AAW92189	Analogue of parath
529	16	47.1	34	20	AAW92190	Analogue of parath
530	16	47.1	34	20	AAW92191	Analogue of parath
531	16	47.1	34	20	AAW92192	Analogue of parath
532	16	47.1	34	20	AAW92193	Analogue of parath
533	16	47.1	34	20	AAW92194	Analogue of parath
534	16	47.1	34	20	AAW92195	Analogue of parath
535	16	47.1	34	20	AAW92196	Analogue of parath
536	16	47.1	34	20	AAW92197	Analogue of parath
537	16	47.1	34	20	AAW92166	Analogue of parath
538	16	47.1	34	20	AAW92168	Analogue of parath
539	16	47.1	34	20	AAW92169	Analogue of parath
540	16	47.1	34	20	AAW92170	Analogue of parath
541	16	47.1	34	20	AAW92171	Analogue of parath
542	16	47.1	34	20	AAW92172	Analogue of parath
543	16	47.1	34	20	AAW92173	Analogue of parath
544	16	47.1	34	20	AAW92174	Analogue of parath
545	16	47.1	34	20	AAW92175	Analogue of parath
546	16	47.1	34	20	AAW92176	Analogue of parath
547	16	47.1	34	20	AAW92177	Analogue of parath
548	16	47.1	34	20	AAW92178	Analogue of parath
549	16	47.1	34	20	AAW92179	Analogue of parath
550	16	47.1	34	20	AAW92180	Analogue of parath
551	16	47.1	34	20	AAW92181	Analogue of parath
552	16	47.1	34	20	AAW92182	Analogue of parath
553	16	47.1	34	20	AAW92152	Analogue of parath
554	16	47.1	34	20	AAW92150	Analogue of parath
555	16	47.1	34	20	AAW92151	Analogue of parath
556	16	47.1	34	20	AAW92153	Analogue of parath
557	16	47.1	34	20	AAW92154	Analogue of parath
558	16	47.1	34	20	AAW92155	Analogue of parath
559	16	47.1	34	20	AAW92156	Analogue of parath
560	16	47.1	34	20	AAW92157	Analogue of parath
561	16	47.1	34	20	AAW92158	Analogue of parath
562	16	47.1	34	20	AAW92159	Analogue of parath
563	16	47.1	34	20	AAW92160	Analogue of parath

564	16	47.1	34	20	AAW92161	Analogue of parath
565	16	47.1	34	20	AAW92162	Analogue of parath
566	16	47.1	34	20	AAW92163	Analogue of parath
567	16	47.1	34	20	AAW92164	Analogue of parath
568	16	47.1	34	20	AAW92165	Analogue of parath
569	16	47.1	34	20	AAW92148	Analogue of parath
570	16	47.1	34	20	AAW92149	Analogue of parath
571	16	47.1	34	20	AAW81873	Porcine PTH N-term
572	16	47.1	34	21	ABJ10735	Human parathyroid
573	16	47.1	34	21	ABJ10739	Human parathyroid
574	16	47.1	34	21	ABJ10740	Human parathyroid
575	16	47.1	34	21	ABJ10742	Human parathyroid
576	16	47.1	34	21	ABJ10743	Human parathyroid
577	16	47.1	34	22	AAB91084	Parathyroid hormon
578	16	47.1	34	22	AAB91085	Parathyroid hormon
579	16	47.1	34	22	AAB91087	Parathyroid hormon
580	16	47.1	34	23	AAU73036	Parathyroid hormon
581	16	47.1	35	2	AAP10140	h-PTH antigen. Sy
582	16	47.1	36	15	AAR58277	[Nle18]-hPTH(1-36)
583	16	47.1	36	15	AAR58183	[Gln18]-hPTH(1-36)
584	16	47.1	36	15	AAR58184	[Tyr18]-hPTH(1-36)
585	16	47.1	36	15	AAR58042	[L8,D10,K11,L18]-h
586	16	47.1	36	15	AAR58044	[L8,D10,K11,A17,L1
587	16	47.1	36	15	AAR58055	[L8,Q18]-hPTH(1-36
588	16	47.1	36	15	AAR58057	[L8,D10,A16,Q18]-h
589	16	47.1	36	15	AAR58071	[Aib3, Gln18]-hPTH
590	16	47.1	36	15	AAR55820	[L8,D10,K11,Q18]-h
591	16	47.1	36	15	AAR55824	[L8,D10,K11,A16,Q1
592	16	47.1	36	15	AAR58027	[A1,A3,L8,Q18]-hPT
593	16	47.1	36	15	AAR58031	[L8,K11,Q18]-hPTH(
594	16	47.1	36	15	AAR58072	Isopropyl-[L8,D10,
595	16	47.1	36	15	AAR58074	[L8,Y18]-hPTH(1-36
596	16	47.1	36	15	AAR58088	[1-amino-cyclopent
597	16	47.1	37	22	AAB86232	Porcine parathyroi
598	16	47.1	38	15	AAR58159	[Val28]-hPTH(1-38)
599	16	47.1	38	15	AAR58160	[Ile28]-hPTH(1-38)
600	15	44.1	28	13	AAR22061	Modified [Nle_8,18
601	15	44.1	28	13	AAR22062	Modified [Nle_8,18
602	15	44.1	28	13	AAR22067	Modified [Nle_8,_1
603	15	44.1	28	13	AAR22068	Modified [Nle_8,_1
604	15	44.1	28	17	AAR88838	Human parathyroid
605	15	44.1	28	21	ABJ10774	Human parathyroid
606	15	44.1	28	22	AAB81074	Human parathyroid
607	15	44.1	28	23	AAE18404	Bovine PTH peptide
608	15	44.1	28	23	AAU73045	Parathyroid hormon
609	15	44.1	28	23	AAU73048	Parathyroid hormon
610	15	44.1	28	23	AAU73049	Parathyroid hormon
611	15	44.1	29	17	AAR88839	Human parathyroid
612	15	44.1	29	22	AAB81075	Human parathyroid
613	15	44.1	30	17	AAR88833	Human parathyroid
614	15	44.1	30	19	AAW42052	Human parathyroid
615	15	44.1	30	22	AAB91089	Parathyroid hormon
616	15	44.1	30	22	AAB91092	Parathyroid hormon
617	15	44.1	30	23	AAU73062	Parathyroid hormon
618	15	44.1	31	5	AAP40511	Bovine parathyroid
619	15	44.1	31	5	AAP40761	Human parathyroid
620	15	44.1	31	17	AAR88831	Human parathyroid

621	15	44.1	31	19	AAW42056	Human parathyroid
622	15	44.1	31	19	AAW42057	Human parathyroid
623	15	44.1	31	19	AAW42060	Human parathyroid
624	15	44.1	31	19	AAW42062	Human parathyroid
625	15	44.1	31	19	AAW42067	Human parathyroid
626	15	44.1	31	19	AAW42049	Human parathyroid
627	15	44.1	31	19	AAW42050	Human parathyroid
628	15	44.1	31	19	AAW42053	Human parathyroid
629	15	44.1	31	21	AAV96975	Parathyroid hormon
630	15	44.1	31	23	AAU73040	Parathyroid hormon
631	15	44.1	31	23	AAU82640	Analogue of human
632	15	44.1	32	22	AAB91088	Parathyroid hormon
633	15	44.1	32	22	AAB91090	Parathyroid hormon
634	15	44.1	32	22	AAB91091	Parathyroid hormon
635	15	44.1	32	23	AAE18403	Bovine PTH peptide
636	15	44.1	32	23	AAU73041	Parathyroid hormon
637	15	44.1	32	23	AAU73043	Parathyroid hormon
638	15	44.1	34	6	AAP50517	Sequence of methio
639	15	44.1	34	11	AAR07924	Bovine parathyroid
640	15	44.1	34	11	AAR07925	Human parathyroid
641	15	44.1	34	11	AAR08305	Bovine parathyroid
642	15	44.1	34	11	AAR08306	Human parathyroid
643	15	44.1	34	13	AAR22298	Human parathyroid
644	15	44.1	34	13	AAR22299	Human parathyroid
645	15	44.1	34	14	AAR41554	[Thr27]hPTH (1-34)
646	15	44.1	34	14	AAR41555	[Asn27]hPTH (1-34)
647	15	44.1	34	14	AAR41558	[Ser27]hPTH (1-34)
648	15	44.1	34	14	AAR41559	[Gly27]hPTH (1-34)
649	15	44.1	34	14	AAR41560	[His27]hPTH (1-34)
650	15	44.1	34	15	AAR45528	Parathyroid hormon
651	15	44.1	34	16	AAR69055	PTH analogue with
652	15	44.1	34	17	AAR88829	Human parathyroid
653	15	44.1	34	17	AAR88834	Human parathyroid
654	15	44.1	34	18	AAW13352	Truncated parathyr
655	15	44.1	34	18	AAW12651	Parathyroid hormon
656	15	44.1	34	18	AAW08130	Human PTH derivati
657	15	44.1	34	18	AAW20004	Cyclised [Nle 8,18
658	15	44.1	34	18	AAW19997	Cyclised [Nle 8,18
659	15	44.1	34	18	AAW19998	Cyclised [Nle 8,18
660	15	44.1	34	18	AAW20003	Cyclised [Nle 8,18
661	15	44.1	34	18	AAW20009	Cyclised [Nle 8,18
662	15	44.1	34	18	AAW20010	Cyclised [Nle 8,18
663	15	44.1	34	18	AAW17940	Human PTH analogue
664	15	44.1	34	18	AAW17969	Human parathyroid
665	15	44.1	34	18	AAW17970	Human PTH analogue
666	15	44.1	34	18	AAW17964	Human PTH analogue
667	15	44.1	34	18	AAW17954	Human parathyroid
668	15	44.1	34	18	AAW17956	Human parathyroid
669	15	44.1	34	18	AAW17962	Human PTH analogue
670	15	44.1	34	19	AAW67275	Parathyroid hormon
671	15	44.1	34	19	AAW67292	Parathyroid hormon
672	15	44.1	34	19	AAW67297	Parathyroid hormon
673	15	44.1	34	19	AAW61725	Parathyroid hormon
674	15	44.1	34	19	AAW66053	Parathyroid hormon
675	15	44.1	34	19	AAW42602	Parathyroid hormon
676	15	44.1	34	19	AAW42054	Human parathyroid
677	15	44.1	34	19	AAW42055	Human parathyroid

678	15	44.1	34	19	AAW48395	Human PTH/PTHrP hy
679	15	44.1	34	20	AAW74396	Modified parathyro
680	15	44.1	34	20	AAW81945	Synthetic PTH and
681	15	44.1	34	21	ABJ10705	Human parathyroid
682	15	44.1	34	21	ABJ10707	Human parathyroid
683	15	44.1	34	21	ABJ10708	Human parathyroid
684	15	44.1	34	21	ABJ10709	Human parathyroid
685	15	44.1	34	21	ABJ10710	Human parathyroid
686	15	44.1	34	21	ABJ10711	Human parathyroid
687	15	44.1	34	21	ABJ10715	Human parathyroid
688	15	44.1	34	21	ABJ10716	Human parathyroid
689	15	44.1	34	21	ABJ10718	Human parathyroid
690	15	44.1	34	21	ABJ10720	Human parathyroid
691	15	44.1	34	21	ABJ10721	Human parathyroid
692	15	44.1	34	21	ABJ10723	Human parathyroid
693	15	44.1	34	21	ABJ10725	Human parathyroid
694	15	44.1	34	21	ABJ10726	Human parathyroid
695	15	44.1	34	21	ABJ10728	Human parathyroid
696	15	44.1	34	21	ABJ10731	Human parathyroid
697	15	44.1	34	21	ABJ10732	Human parathyroid
698	15	44.1	34	21	ABJ10734	Human parathyroid
699	15	44.1	34	21	ABJ10738	Human parathyroid
700	15	44.1	34	21	ABJ10741	Human parathyroid
701	15	44.1	34	21	ABJ10744	Human parathyroid
702	15	44.1	34	21	ABJ10745	Human parathyroid
703	15	44.1	34	21	ABJ10746	Human parathyroid
704	15	44.1	34	21	ABJ10747	Human parathyroid
705	15	44.1	34	21	ABJ10748	Human parathyroid
706	15	44.1	34	21	ABJ10749	Human parathyroid
707	15	44.1	34	21	ABJ10750	Human parathyroid
708	15	44.1	34	21	ABJ10751	Human parathyroid
709	15	44.1	34	21	ABJ10752	Human parathyroid
710	15	44.1	34	21	ABJ10753	Human parathyroid
711	15	44.1	34	21	ABJ10754	Human parathyroid
712	15	44.1	34	21	ABJ10755	Human parathyroid
713	15	44.1	34	21	ABJ10756	Human parathyroid
714	15	44.1	34	21	ABJ10761	Human parathyroid
715	15	44.1	34	21	ABJ10762	Human parathyroid
716	15	44.1	34	21	ABJ10763	Human parathyroid
717	15	44.1	34	21	ABJ10764	Human parathyroid
718	15	44.1	34	21	ABJ10765	Human parathyroid
719	15	44.1	34	21	ABJ10766	Human parathyroid
720	15	44.1	34	21	ABJ10767	Human parathyroid
721	15	44.1	34	21	ABJ10768	Human parathyroid
722	15	44.1	34	21	ABJ10770	Human parathyroid
723	15	44.1	34	21	ABJ10771	Human parathyroid
724	15	44.1	34	21	ABJ10777	Human parathyroid
725	15	44.1	34	23	AAE18396	Bovine PTH peptide
726	15	44.1	34	23	AAE18397	Human PTH peptide
727	15	44.1	34	23	AAU73031	Parathyroid hormon
728	15	44.1	34	23	AAU73033	Parathyroid hormon
729	15	44.1	34	23	AAU73035	Parathyroid hormon
730	15	44.1	35	16	AAR74518	Parathyroid hormon
731	15	44.1	35	16	AAR74519	Parathyroid hormon
732	15	44.1	35	16	AAR74520	Parathyroid hormon
733	15	44.1	35	16	AAR74527	Human parathyroid
734	15	44.1	35	16	AAR74464	Parathyroid hormon

735	15	44.1	35	16	AAR74465	Parathyroid hormon
736	15	44.1	35	16	AAR74466	Parathyroid hormon
737	15	44.1	35	16	AAR74467	Parathyroid hormon
738	15	44.1	35	16	AAR74468	Parathyroid hormon
739	15	44.1	35	16	AAR74469	Parathyroid hormon
740	15	44.1	35	16	AAR74470	Parathyroid hormon
741	15	44.1	35	16	AAR74471	Parathyroid hormon
742	15	44.1	35	16	AAR74472	Parathyroid hormon
743	15	44.1	35	16	AAR74473	Parathyroid hormon
744	15	44.1	35	16	AAR74474	Parathyroid hormon
745	15	44.1	35	16	AAR74475	Parathyroid hormon
746	15	44.1	35	16	AAR74476	Parathyroid hormon
747	15	44.1	35	16	AAR74477	Parathyroid hormon
748	15	44.1	35	16	AAR74478	Parathyroid hormon
749	15	44.1	35	16	AAR74479	Parathyroid hormon
750	15	44.1	35	16	AAR74448	Parathyroid hormon
751	15	44.1	35	16	AAR74449	Parathyroid hormon
752	15	44.1	35	16	AAR74450	Parathyroid hormon
753	15	44.1	35	16	AAR74451	Parathyroid hormon
754	15	44.1	35	16	AAR74452	Parathyroid hormon
755	15	44.1	35	16	AAR74453	Parathyroid hormon
756	15	44.1	35	16	AAR74454	Parathyroid hormon
757	15	44.1	35	16	AAR74455	Parathyroid hormon
758	15	44.1	35	16	AAR74456	Parathyroid hormon
759	15	44.1	35	16	AAR74457	Parathyroid hormon
760	15	44.1	35	16	AAR74458	Parathyroid hormon
761	15	44.1	35	16	AAR74459	Parathyroid hormon
762	15	44.1	35	16	AAR74460	Parathyroid hormon
763	15	44.1	35	16	AAR74461	Parathyroid hormon
764	15	44.1	35	16	AAR74462	Parathyroid hormon
765	15	44.1	35	16	AAR74463	Parathyroid hormon
766	15	44.1	35	16	AAR74432	Parathyroid hormon
767	15	44.1	35	16	AAR74433	Parathyroid hormon
768	15	44.1	35	16	AAR74434	Parathyroid hormon
769	15	44.1	35	16	AAR74435	Parathyroid hormon
770	15	44.1	35	16	AAR74436	Parathyroid hormon
771	15	44.1	35	16	AAR74437	Parathyroid hormon
772	15	44.1	35	16	AAR74438	Parathyroid hormon
773	15	44.1	35	16	AAR74439	Parathyroid hormon
774	15	44.1	35	16	AAR74440	Parathyroid hormon
775	15	44.1	35	16	AAR74441	Parathyroid hormon
776	15	44.1	35	16	AAR74442	Parathyroid hormon
777	15	44.1	35	16	AAR74443	Parathyroid hormon
778	15	44.1	35	16	AAR74444	Parathyroid hormon
779	15	44.1	35	16	AAR74445	Parathyroid hormon
780	15	44.1	35	16	AAR74446	Parathyroid hormon
781	15	44.1	35	16	AAR74447	Parathyroid hormon
782	15	44.1	35	16	AAR74429	Parathyroid hormon
783	15	44.1	35	16	AAR74430	Parathyroid hormon
784	15	44.1	35	16	AAR74431	Parathyroid hormon
785	15	44.1	35	16	AAR74398	Parathyroid hormon
786	15	44.1	35	16	AAR74399	Parathyroid hormon
787	15	44.1	35	16	AAR74400	Parathyroid hormon
788	15	44.1	35	16	AAR74394	Parathyroid hormon
789	15	44.1	35	16	AAR74395	Parathyroid hormon
790	15	44.1	35	16	AAR74396	Parathyroid hormon
791	15	44.1	35	16	AAR74397	Parathyroid hormon

792	15	44.1	35	23	AAU73175	Parathyroid hormon
793	15	44.1	36	15	AAR58222	[His27]-hPTH(1-36)
794	15	44.1	36	15	AAR58223	[Phe27]-hPTH(1-36)
795	15	44.1	36	15	AAR58224	[Nle27]-hPTH(1-36)
796	15	44.1	36	15	AAR58225	[Asn27]-hPTH(1-36)
797	15	44.1	36	15	AAR58226	[Ala27]-hPTH(1-36)
798	15	44.1	36	15	AAR58214	[Ala19]-hPTH(1-36)
799	15	44.1	36	15	AAR58041	[L8,D10,K11,S14,I1
800	15	44.1	36	15	AAR58043	[L8,Q16,D17,L18,R1
801	15	44.1	36	15	AAR58046	[L8,A16,D17,L18,A1
802	15	44.1	36	15	AAR58047	[L8,D10,A16,D17,L1
803	15	44.1	36	15	AAR58050	[L8,A16,D17,Q18,A1
804	15	44.1	36	15	AAR58051	[L8,A16,A17,Q18,A1
805	15	44.1	36	15	AAR58052	[L8,A17,Q18,A19]-h
806	15	44.1	36	15	AAR58067	[L8,A16,A17,A18,A1
807	15	44.1	36	15	AAR58069	Isopropyl-[L8,K(Is
808	15	44.1	36	15	AAR58070	Isopropyl-[L8,K(Is
809	15	44.1	36	15	AAR55822	[L8,D10,K11,A16,Q1
810	15	44.1	36	15	AAR55825	[L8,A16,Q18,A19]-h
811	15	44.1	36	15	AAR58086	[1-amino-cyclopent
812	15	44.1	38	15	AAR58136	[Arg19]-hPTH(1-38)
813	15	44.1	38	15	AAR58154	[Val27]-hPTH(1-38)
814	15	44.1	38	15	AAR58155	[Ile27]-hPTH(1-38)
815	15	44.1	38	15	AAR58156	[Leu27]-hPTH(1-38)
816	15	44.1	38	15	AAR58157	[Arg27]-hPTH(1-38)
817	15	44.1	38	15	AAR58158	[Ala27]-hPTH(1-38)
818	15	44.1	38	15	AAR58123	[Ser19]-hPTH(1-38)
819	15	44.1	38	15	AAR58124	[Lys19]-hPTH(1-38)
820	15	44.1	38	15	AAR58125	[Leu19]-hPTH(1-38)
821	15	44.1	38	15	AAR58126	[Ala19]-hPTH(1-38)
822	15	44.1	38	15	AAR58127	[Tyr19]-hPTH(1-38)
823	15	44.1	38	15	AAR58128	[Met19]-hPTH(1-38)
824	15	44.1	38	15	AAR58129	[His19]-hPTH(1-38)
825	15	44.1	38	15	AAR58130	[Val19]-hPTH(1-38)
826	15	44.1	38	15	AAR58131	[Gly19]-hPTH(1-38)
827	15	44.1	38	15	AAR58132	[Pro19]-hPTH(1-38)
828	15	44.1	38	15	AAR58133	[Asp19]-hPTH(1-38)
829	15	44.1	38	15	AAR58134	[Ile19]-hPTH(1-38)
830	14	41.2	28	23	AAU73066	Parathyroid hormon
831	14	41.2	30	23	AAU73057	Parathyroid hormon
832	14	41.2	33	17	AAW15814	[Leu(8),Trp(10),Al
833	14	41.2	34	14	AAR41556	[Gln26,27]hPTH (1-
834	14	41.2	34	14	AAR41566	[Arg 26,27]hPTH (1
835	14	41.2	34	14	AAR41567	[Gln26]hPTH (1-34)
836	14	41.2	34	15	AAR55817	[L8,Q18,T33,A34]-h
837	14	41.2	34	15	AAR55819	[L8,A16,Q18,T33,A3
838	14	41.2	34	15	AAR55821	[L8,D10,K11,Q18,T3
839	14	41.2	34	15	AAR55823	[L8,D10,K11,A16,Q1
840	14	41.2	34	15	AAR58021	[L8,D10,A16,Q18,T3
841	14	41.2	34	15	AAR58034	Isopropyl-[L8,K(Is
842	14	41.2	34	17	AAW15813	[Leu(8),Trp(10),Al
843	14	41.2	34	17	AAW15815	[Leu(8),Trp(10),DL
844	14	41.2	34	17	AAW15828	N-alpha-acylated [
845	14	41.2	34	18	AAW08132	Human PTH derivati
846	14	41.2	34	18	AAW17960	Human PTH analogue
847	14	41.2	34	20	AAV02587	Parathyroid hormon
848	14	41.2	34	21	ABJ10757	Human parathyroid

849	14	41.2	35	16	AAR74515	Parathyroid hormon
850	14	41.2	35	16	AAR74516	Parathyroid hormon
851	14	41.2	35	16	AAR74517	Parathyroid hormon
852	14	41.2	35	16	AAR74480	Parathyroid hormon
853	14	41.2	35	16	AAR74401	Parathyroid hormon
854	14	41.2	35	16	AAR74409	Parathyroid hormon
855	14	41.2	35	16	AAR74412	Parathyroid hormon
856	14	41.2	36	15	AAR58290	[Ala26]-hPTH(1-36)
857	14	41.2	36	15	AAR58279	[Lys20]-hPTH(1-36)
858	14	41.2	36	15	AAR58218	[Gln26]-hPTH(1-36)
859	14	41.2	36	15	AAR58219	[Nle26]-hPTH(1-36)
860	14	41.2	38	15	AAR58137	[Phe20]-hPTH(1-38)
861	14	41.2	38	15	AAR58153	[Arg26]-hPTH(1-38)
862	13	38.2	32	22	AAB84835	Parathyroid hormon
863	13	38.2	32	22	AAB96906	Parathyroid hormon
864	13	38.2	34	13	AAR22297	Human parathyroid
865	13	38.2	34	14	AAR34456	Human parathyroid
866	13	38.2	34	14	AAR34457	Human parathyroid
867	13	38.2	34	14	AAR41557	[Gln25,26,27]hPTH
868	13	38.2	34	15	AAR58195	[S14,I15,Q16,D17,L
869	13	38.2	34	15	AAR58045	[L8,Q16,D17,L18,R1
870	13	38.2	34	15	AAR58049	[L8,D10,K11,Q16,D1
871	13	38.2	34	15	AAR58056	[L8,D10,K11,A16,Q1
872	13	38.2	34	15	AAR58058	[L8,D10,K11,A16,Q1
873	13	38.2	34	15	AAR55818	[L8,A16,Q18,A19,T3
874	13	38.2	34	18	AAW08131	Human PTH derivati
875	13	38.2	34	21	ABJ10758	Human parathyroid
876	13	38.2	34	22	AAB84828	Parathyroid hormon
877	13	38.2	34	22	AAB96921	Parathyroid hormon
878	13	38.2	35	16	AAR74512	Parathyroid hormon
879	13	38.2	35	16	AAR74513	Parathyroid hormon
880	13	38.2	35	16	AAR74514	Parathyroid hormon
881	13	38.2	35	16	AAR74511	Parathyroid hormon
882	13	38.2	35	16	AAR74481	Parathyroid hormon
883	13	38.2	35	16	AAR74482	Parathyroid hormon
884	13	38.2	35	16	AAR74483	Parathyroid hormon
885	13	38.2	35	16	AAR74408	Parathyroid hormon
886	13	38.2	36	15	AAR58287	[Phe25]-hPTH(1-36)
887	13	38.2	36	15	AAR58288	[Lys25]-hPTH(1-36)
888	13	38.2	36	15	AAR58289	[Ala25]-hPTH(1-36)
889	13	38.2	36	15	AAR58192	[Gln25]-hPTH(1-36)
890	13	38.2	36	15	AAR58216	[Ala21]-hPTH(1-36)
891	13	38.2	38	15	AAR58138	[Ala21]-hPTH(1-38)
892	13	38.2	38	15	AAR58139	[Gly21]-hPTH(1-38)
893	13	38.2	38	15	AAR58140	[Phe21]-hPTH(1-38)
894	13	38.2	38	15	AAR58141	[Leu21]-hPTH(1-38)
895	13	38.2	38	15	AAR58142	[Asn21]-hPTH(1-38)
896	13	38.2	38	15	AAR58143	[Gln21]-hPTH(1-38)
897	13	38.2	38	15	AAR58144	[Ser21]-hPTH(1-38)
898	12	35.3	28	23	AAU73065	Parathyroid hormon
899	12	35.3	28	23	AAU73067	Parathyroid hormon
900	12	35.3	29	13	AAR22070	Modified rPTH(7-34
901	12	35.3	30	23	AAU73056	Parathyroid hormon
902	12	35.3	30	23	AAU73058	Parathyroid hormon
903	12	35.3	30	23	AAU73059	Parathyroid hormon
904	12	35.3	34	11	AAR07917	Rat parathyroid ho
905	12	35.3	34	11	AAR08298	Rat parathyroid ho

906	12	35.3	34	16	AAR62432	Accelerator peptid
907	12	35.3	34	17	AAR99980	Rat parathyroid ho
908	12	35.3	34	18	AAW19996	Cyclised rat parat
909	12	35.3	34	18	AAW20002	Cyclised rat parat
910	12	35.3	34	18	AAW20008	Cyclised rat parat
911	12	35.3	34	18	AAW17949	Human parathyroid
912	12	35.3	34	18	AAW17945	Human parathyroid
913	12	35.3	34	18	AAW17950	Human PTH analogue
914	12	35.3	34	19	AAW67280	Parathyroid hormon
915	12	35.3	34	19	AAW67284	Parathyroid hormon
916	12	35.3	34	19	AAW67285	Parathyroid hormon
917	12	35.3	34	19	AAW67288	Parathyroid hormon
918	12	35.3	34	19	AAW67289	Parathyroid hormon
919	12	35.3	34	19	AAW67294	Parathyroid hormon
920	12	35.3	34	19	AAW67295	Parathyroid hormon
921	12	35.3	34	19	AAW67296	Parathyroid hormon
922	12	35.3	34	19	AAW67303	Parathyroid hormon
923	12	35.3	34	19	AAW67304	Parathyroid hormon
924	12	35.3	34	19	AAW48396	Human PTH/PTHrP hy
925	12	35.3	34	21	ABJ10759	Human parathyroid
926	12	35.3	34	22	AAB84777	Native human parat
927	12	35.3	34	22	AAB96897	Rat parathyroid ho
928	12	35.3	34	22	AAB91100	Parathyroid hormon
929	12	35.3	34	23	AAU73037	Parathyroid hormon
930	12	35.3	34	24	ABP71499	Rat parathyroid ho
931	12	35.3	35	16	AAR74507	Parathyroid hormon
932	12	35.3	35	16	AAR74508	Parathyroid hormon
933	12	35.3	35	16	AAR74509	Parathyroid hormon
934	12	35.3	35	16	AAR74510	Parathyroid hormon
935	12	35.3	35	16	AAR74484	Parathyroid hormon
936	12	35.3	35	16	AAR74485	Parathyroid hormon
937	12	35.3	35	16	AAR74486	Parathyroid hormon
938	12	35.3	36	15	AAR58208	[A13,Q26,F27,D-F34
939	12	35.3	36	15	AAR58217	[Ala22]-hPTH(1-36)
940	12	35.3	36	15	AAR58053	[L8,A17,Q18,A19,R2
941	12	35.3	36	15	AAR58060	[L8,A16,Q18,A19,R2
942	12	35.3	36	15	AAR58064	[L8,S13,A16,Q18,A1
943	12	35.3	36	15	AAR58032	[L8,A16,D17,L18,R1
944	12	35.3	36	15	AAR58073	Isopropyl-[L8,S13,
945	12	35.3	37	22	AAB86231	Rat parathyroid ho
946	12	35.3	38	15	AAR58145	[Gly22]-hPTH(1-38)
947	12	35.3	38	15	AAR58146	[Leu22]-hPTH(1-38)
948	12	35.3	38	15	AAR58147	[His22]-hPTH(1-38)
949	12	35.3	38	15	AAR58148	[Ala22]-hPTH(1-38)
950	12	35.3	38	15	AAR58149	[Ile22]-hPTH(1-38)
951	12	35.3	38	15	AAR58150	[Val22]-hPTH(1-38)
952	12	35.3	38	15	AAR58151	[Ser22]-hPTH(1-38)
953	12	35.3	38	15	AAR58152	[Arg22]-hPTH(1-38)
954	11	32.4	28	9	AAP82184	Sequence of parath
955	11	32.4	28	13	AAR22071	Modified [Tyr_34]r
956	11	32.4	28	13	AAR22072	Modified [D-Trp_12
957	11	32.4	28	13	AAR22073	Modified [Nle_8,_1
958	11	32.4	28	13	AAR22074	Modified [Nle_8,_1
959	11	32.4	28	23	AAU73105	Parathyroid hormon
960	11	32.4	28	23	AAU73106	Parathyroid hormon
961	11	32.4	30	22	AAB84834	Parathyroid hormon
962	11	32.4	30	22	AAB96905	Parathyroid hormon

963	11	32.4	30	23	AAU73054	Parathyroid hormon
964	11	32.4	30	23	AAU73136	Parathyroid hormon
965	11	32.4	30	23	AAU73137	Parathyroid hormon
966	11	32.4	32	22	AAB91094	Parathyroid hormon
967	11	32.4	33	9	AAP82176	Sequence of parath
968	11	32.4	34	7	AAP61414	Peptide with parat
969	11	32.4	34	8	AAP71281	Parathyroid hormon
970	11	32.4	34	11	AAR07920	Rat parathyroid ho
971	11	32.4	34	11	AAR07923	Rat parathyroid ho
972	11	32.4	34	11	AAR08301	Rat parathyroid ho
973	11	32.4	34	11	AAR08304	Rat parathyroid ho
974	11	32.4	34	14	AAR34358	Human parathyroid
975	11	32.4	34	14	AAR34337	Bovine parathyroid
976	11	32.4	34	14	AAR34338	Bovine parathyroid
977	11	32.4	34	14	AAR34339	Bovine parathyroid
978	11	32.4	34	14	AAR34340	Bovine parathyroid
979	11	32.4	34	14	AAR34341	Bovine parathyroid
980	11	32.4	34	14	AAR34342	Bovine parathyroid
981	11	32.4	34	14	AAR34343	Bovine parathyroid
982	11	32.4	34	14	AAR34344	Bovine parathyroid
983	11	32.4	34	14	AAR34345	Bovine parathyroid
984	11	32.4	34	14	AAR34346	Bovine parathyroid
985	11	32.4	34	14	AAR34347	Bovine parathyroid
986	11	32.4	34	14	AAR34348	Bovine parathyroid
987	11	32.4	34	14	AAR34349	Bovine parathyroid
988	11	32.4	34	14	AAR34350	Bovine parathyroid
989	11	32.4	34	14	AAR34351	Bovine parathyroid
990	11	32.4	34	14	AAR34352	Bovine parathyroid
991	11	32.4	34	14	AAR34353	Human parathyroid
992	11	32.4	34	14	AAR34354	Human parathyroid
993	11	32.4	34	14	AAR34355	Human parathyroid
994	11	32.4	34	14	AAR34356	Human parathyroid
995	11	32.4	34	14	AAR34357	Human parathyroid
996	11	32.4	34	14	AAR34359	Human parathyroid
997	11	32.4	34	14	AAR34360	Human parathyroid
998	11	32.4	34	14	AAR34361	Human parathyroid
999	11	32.4	34	14	AAR34362	Human parathyroid
1000	11	32.4	34	14	AAR34363	Human parathyroid

ALIGNMENTS

RESULT 1

AAU73029

ID AAU73029 standard; Peptide; 34 AA.

XX

AC AAU73029;

XX

DT 12-MAR-2002 (first entry)

XX

DE Parathyroid hormone PTH/PTHrP modulating domain #11.

XX

KW Human; parathyroid hormone; PTH; parathyroid hormone-related protein;

KW PTHrP; bone resorption inhibitor; osteoprotegerin; OPG; OPG-L antibody;

KW calcitonin; bisphosphonate; oestrogen; oestrogen receptor; tibolone;

KW osteopenia; hyperthyroidism; hypercalcaemia; tumour metastasis; bone;

KW breast cancer; prostate cancer; cachexia; anorexia; osteoporosis;
 KW Paget's disease; osteomyelitis; osteonecrosis; bone cell death;
 KW Gaucher's disease; sickle cell anaemia; systemic lupus erythematosus;
 KW rheumatoid arthritis; periodontal disease; alopecia; fracture repair;
 KW immunoglobulin G; IgG.
 XX
 OS Homo sapiens.
 XX
 PN WO200181415-A2.
 XX
 PD 01-NOV-2001.
 XX
 PF 27-APR-2001; 2001WO-US13528.
 XX
 PR 27-APR-2000; 2000US-200053P.
 PR 28-JUN-2000; 2000US-214860P.
 PR 06-FEB-2001; 2001US-266673P.
 PR 26-APR-2001; 2001US-0843221.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Kostenuik P, Liu C, Lacey DL;
 XX
 DR WPI; 2002-066435/09.
 XX
 PT Composition, useful for treating osteopenia, comprises parathyroid
 PT hormone and parathyroid hormone-related protein receptor modulators -
 XX
 PS Claim 39; Page 26; 107pp; English.
 XX
 CC The invention relates to a composition (I) comprising modulators of
 CC parathyroid hormone (PTH) and parathyroid hormone-related protein (PTHrP)
 CC which comprise a PTH/PTHrP modulating domain and a vehicle. (I)
 CC comprising PTH agonist optionally with a bone resorption inhibitor, such
 CC as osteoprotegrin (OPG), OPG-L antibody, calcitonin, bisphosphonates,
 CC oestrogens, oestrogen receptor modulators and tibolone is useful for
 CC treating osteopenia. (I) is useful for therapeutic and prophylactic
 CC purposes. Antagonists of PTH receptor are useful in treating primary and
 CC secondary hyperthyroidism, hypercalcaemia, tumour metastases,
 CC particularly breast and prostate cancer, cachexia and anorexia,
 CC osteopenia, including various forms of osteoporosis, Paget's disease of
 CC bone, osteomyelitis, osteonecrosis or bone cell death, associated with
 CC traumatic injury or nontraumatic necrosis associated with Gaucher's
 CC disease, sickle cell anaemia, systemic lupus erythematosus, rheumatoid
 CC arthritis, periodontal disease and alopecia. PTH receptor agonists are
 CC useful as therapeutic agents in conditions including fracture repair
 CC (including healing of non-union fractures), osteopenia, including various
 CC forms of osteoporosis. AAU73018-AAU73181 represent parathyroid hormone
 CC and parathyroid hormone related protein (PTH/PTHrP) modulators and
 CC related amino acid sequences of the invention.
 XX
 SQ Sequence 34 AA;

Query Match 100.0%; Score 34; DB 23; Length 34;
 Best Local Similarity 100.0%; Pred. No. 8.1e-29;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNRGKHLNSMERVEWLRKKLQDVHNF 34
|||||
Db 1 SVSEIQLMHNRGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 2

AAU73173

ID AAU73173 standard; Peptide; 35 AA.

XX

AC AAU73173;

XX

DT 12-MAR-2002 (first entry)

XX

DE Parathyroid hormone PTH/PTHrP modulating domain #155.

XX

KW Human; parathyroid hormone; PTH; parathyroid hormone-related protein;
KW PTHrP; bone resorption inhibitor; osteoprotegrin; OPG; OPG-L antibody;
KW calcitonin; bisphosphonate; oestrogen; oestrogen receptor; tibolone;
KW osteopenia; hyperthyroidism; hypercalcaemia; tumour metastasis; bone;
KW breast cancer; prostate cancer; cachexia; anorexia; osteoporosis;
KW Paget's disease; osteomyelitis; osteonecrosis; bone cell death;
KW Gaucher's disease; sickle cell anaemia; systemic lupus erythematosus;
KW rheumatoid arthritis; periodontal disease; alopecia; fracture repair;
KW immunoglobulin G; IgG.

XX

OS Synthetic.

XX

PN WO200181415-A2.

XX

PD 01-NOV-2001.

XX

PF 27-APR-2001; 2001WO-US13528.

XX

PR 27-APR-2000; 2000US-200053P.

PR 28-JUN-2000; 2000US-214860P.

PR 06-FEB-2001; 2001US-266673P.

PR 26-APR-2001; 2001US-0843221.

XX

PA (AMGE-) AMGEN INC.

XX

PI Kostenuik P, Liu C, Lacey DL;

XX

DR WPI; 2002-066435/09.

XX

PT Composition, useful for treating osteopenia, comprises parathyroid
PT hormone and parathyroid hormone-related protein receptor modulators -

XX

PS Disclosure; Page 63; 107pp; English.

XX

CC The invention relates to a composition (I) comprising modulators of
CC parathyroid hormone (PTH) and parathyroid hormone-related protein (PTHrP)
CC which comprise a PTH/PTHrP modulating domain and a vehicle. (I)
CC comprising PTH agonist optionally with a bone resorption inhibitor, such
CC as osteoprotegrin (OPG), OPG-L antibody, calcitonin, bisphosphonates,
CC oestrogens, oestrogen receptor modulators and tibolone is useful for
CC treating osteopenia. (I) is useful for therapeutic and prophylactic
CC purposes. Antagonists of PTH receptor are useful in treating primary and

CC secondary hyperthyroidism, hypercalcaemia, tumour metastases,
CC particularly breast and prostate cancer, cachexia and anorexia,
CC osteopenia, including various forms of osteoporosis, Paget's disease of
CC bone, osteomyelitis, osteonecrosis or bone cell death, associated with
CC traumatic injury or nontraumatic necrosis associated with Gaucher's
CC disease, sickle cell anaemia, systemic lupus erythematosus, rheumatoid
CC arthritis, periodontal disease and alopecia. PTH receptor agonists are
CC useful as therapeutic agents in conditions including fracture repair
CC (including healing of non-union fractures), osteopenia, including various
CC forms of osteoporosis. AAU73018-AAU73181 represent parathyroid hormone
CC and parathyroid hormone related protein (PTH/PTHrP) modulators and
CC related amino acid sequences of the invention.

XX

SQ Sequence 35 AA;

Query Match 100.0%; Score 34; DB 23; Length 35;
Best Local Similarity 100.0%; Pred. No. 8.3e-29;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNRGKHLNSMERVEWLRKKLQDVHNF 34

|||||

Db 1 SVSEIQLMHNRGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 3

AAU73052

ID AAU73052 standard; Peptide; 30 AA.

XX

AC AAU73052;

XX

DT 12-MAR-2002 (first entry)

XX

DE Parathyroid hormone PTH/PTHrP modulating domain #34.

XX

KW Human; parathyroid hormone; PTH; parathyroid hormone-related protein;

KW PTHrP; bone resorption inhibitor; osteoprotegrin; OPG; OPG-L antibody;

KW calcitonin; bisphosphonate; oestrogen; oestrogen receptor; tibolone;

KW osteopenia; hyperthyroidism; hypercalcaemia; tumour metastasis; bone;

KW breast cancer; prostate cancer; cachexia; anorexia; osteoporosis;

KW Paget's disease; osteomyelitis; osteonecrosis; bone cell death;

KW Gaucher's disease; sickle cell anaemia; systemic lupus erythematosus;

KW rheumatoid arthritis; periodontal disease; alopecia; fracture repair;

KW immunoglobulin G; IgG.

XX

OS Homo sapiens.

XX

PN WO200181415-A2.

XX

PD 01-NOV-2001.

XX

PF 27-APR-2001; 2001WO-US13528.

XX

PR 27-APR-2000; 2000US-200053P.

PR 28-JUN-2000; 2000US-214860P.

PR 06-FEB-2001; 2001US-266673P.

PR 26-APR-2001; 2001US-0843221.

XX

PA (AMGE-) AMGEN INC.
 XX
 PI Kostenuik P, Liu C, Lacey DL;
 XX
 DR WPI; 2002-066435/09.
 XX
 PT Composition, useful for treating osteopenia, comprises parathyroid
 PT hormone and parathyroid hormone-related protein receptor modulators -
 XX
 PS Disclosure; Page 27; 107pp; English.
 XX
 CC The invention relates to a composition (I) comprising modulators of
 CC parathyroid hormone (PTH) and parathyroid hormone-related protein (PTHrP)
 CC which comprise a PTH/PTHrP modulating domain and a vehicle. (I)
 CC comprising PTH agonist optionally with a bone resorption inhibitor, such
 CC as osteoprotegrin (OPG), OPG-L antibody, calcitonin, bisphosphonates,
 CC oestrogens, oestrogen receptor modulators and tibolone is useful for
 CC treating osteopenia. (I) is useful for therapeutic and prophylactic
 CC purposes. Antagonists of PTH receptor are useful in treating primary and
 CC secondary hyperthyroidism, hypercalcaemia, tumour metastases,
 CC particularly breast and prostate cancer, cachexia and anorexia,
 CC osteopenia, including various forms of osteoporosis, Paget's disease of
 CC bone, osteomyelitis, osteonecrosis or bone cell death, associated with
 CC traumatic injury or nontraumatic necrosis associated with Gaucher's
 CC disease, sickle cell anaemia, systemic lupus erythematosus, rheumatoid
 CC arthritis, periodontal disease and alopecia. PTH receptor agonists are
 CC useful as therapeutic agents in conditions including fracture repair
 CC (including healing of non-union fractures), osteopenia, including various
 CC forms of osteoporosis. AAU73018-AAU73181 represent parathyroid hormone
 CC and parathyroid hormone related protein (PTH/PTHrP) modulators and
 CC related amino acid sequences of the invention.
 XX
 SQ Sequence 30 AA;

Query Match 88.2%; Score 30; DB 23; Length 30;
 Best Local Similarity 100.0%; Pred. No. 1.2e-24;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNRGKHLNSMERVEWLRKKLQD 30
 |||||
 Db 1 SVSEIQLMHNRGKHLNSMERVEWLRKKLQD 30

RESULT 4

AAR22064

ID AAR22064 standard; Protein; 28 AA.
 XX
 AC AAR22064;
 XX
 DT 14-JUL-1992 (first entry)
 XX
 DE Modified hPTH(7-34)NH2.
 XX
 KW Parathyroid hormone; analogue; osteoporosis; hyperthyroidism;
 KW tumours; hypercalcaemia; renal failure; human.
 XX
 OS Synthetic.

XX
 FH Key Location/Qualifiers
 FT Modified-site 7
 FT /label= OTHER
 FT /note= "OTHER = see comments"
 FT Modified-site 28
 FT /label= NH2
 XX
 PN US5093233-A.
 XX
 PD 03-MAR-1992.
 XX
 PF 25-APR-1990; 90US-0514394.
 XX
 PR 25-APR-1990; 90US-0514394.
 XX
 PA (MERI) MERCK & CO INC.
 XX
 PI Rosenblatt M, Roubini E, Chorev M, Nutt RF;
 XX
 DR WPI; 1992-096233/12.
 XX
 PT New parathyroid hormone analogues - useful for treatment and in
 PT vitro diagnosis of PTH-dependent tumours, immune disorders,
 PT osteoporosis and hyperparathyroidism.
 XX
 PS Claim 1; Column 10; 6pp; English.
 XX
 CC The peptide is modified at Lys13 (of the parent PTH) in the epsilon
 CC amino acid gp. by N,N-diisobutyl or 3-phenylpropanoyl. The PTH
 CC analogue binds with high affinity to the peptide hormone receptor
 CC without activating the 2nd messenger mol. The modification of the
 CC Lys residue stabilises the bioactive conformation of PTH to enhance
 CC the activity. The peptide may be used in in vitro bioassays to
 CC measure naturally occurring PTH and to diagnose the etiology of or
 CC to treat osteoporosis or hypercalcaemia. It may also be used to
 CC treat hyperthyroidism and diseases caused by aberrant prodn. of
 CC hormone-like substances, such as tumours. It may also be used to
 CC treat immune diseases such as inflammation. It is prepd. by solid
 CC phase synthesis.
 CC See also AAR22058-75.
 XX
 SQ Sequence 28 AA;

Query Match 67.6%; Score 23; DB 13; Length 28;
 Best Local Similarity 100.0%; Pred. No. 2.9e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 6 GKHLNSMERVEWLRKKLQDVHNF 28

RESULT 5
 ABJ10776
 ID ABJ10776 standard; Peptide; 28 AA.
 XX

AC ABJ10776;
 XX
 DT 02-DEC-2002 (first entry)
 XX
 DE Human parathyroid hormone analogue #72.
 XX
 KW Human; parathyroid hormone; parathyroid hormone-related protein;
 KW PTH; PTHrP; analogue; abnormal CNS function; pancreatic function;
 KW mineral metabolism; male infertility; abnormal blood pressure;
 KW hypothalamic disease.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 2
 FT /note= "D-form residue"
 FT Modified-site 28
 FT /note= "C-terminal amide"
 XX
 PN WO9957139-A2.
 XX
 PD 11-NOV-1999.
 XX
 PF 03-MAY-1999; 99WO-US09521.
 XX
 PR 05-MAY-1998; 98US-0072956.
 XX
 PA (SCRC) SOC CONSEILS RECH & APPL SCI.
 XX
 PI Chorev M, Dong ZX, Rosenblatt M;
 XX
 DR WPI; 2000-038790/03.
 XX
 PT New parathyroid hormone analogs, used for treating e.g. abnormal CNS or
 PT pancreatic functions, abnormal mineral metabolism and homeostasis, male
 PT infertility, abnormal blood pressure or hypothalamic disease -
 XX
 PS Claim 11; Page 40; 49pp; English.
 XX
 CC The present invention provides a number of parathyroid hormone (PTH) or
 CC parathyroid hormone-related protein (PTHrP) analogues. These act as PTH2
 CC receptor agonists or antagonists and can be used in the treatment of
 CC disorders resulting from altered or excessive action of the PTH2
 CC receptor, e.g. abnormal CNS functions, abnormal pancreatic functions,
 CC divergence from normal mineral metabolism and homeostasis, male
 CC infertility, abnormal blood pressure or a hypothalamic disease. The
 CC present sequence is a peptide analogue of the invention.
 XX
 SQ Sequence 28 AA;

Query Match 67.6%; Score 23; DB 21; Length 28;
 Best Local Similarity 100.0%; Pred. No. 2.9e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34
 ||||||||||||||||||

Db

6 GKHLNSMERVEWLRKKLQDVHNF 28

RESULT 6

AAE23734

ID AAE23734 standard; peptide; 28 AA.

XX

AC AAE23734;

XX

DT 10-SEP-2002 (first entry)

XX

DE Human parathyroid hormone (hPTH) peptide (7-34).

XX

KW Human parathyroid hormone; hPTH; PTH-related peptide; PTHrP; eczema;
KW hyperproliferative skin disorder; psoriasis; ichthyosis; skin cancer;
KW acne; actinic keratosis; alopecia; gene therapy.

XX

OS Homo sapiens.

XX

PN WO200228420-A2.

XX

PD 11-APR-2002.

XX

PF 05-OCT-2001; 2001WO-US31082.

XX

PR 06-OCT-2000; 2000US-238134P.

XX

PA (HOLI/) HOLICK M F.

XX

PI Holick MF;

XX

DR WPI; 2002-452304/48.

DR N-PSDB; AAD37995.

XX

PT Regulating mammalian skin or hair cell proliferation and
PT differentiation by administering nucleic acids encoding peptides
PT derived from N-terminal region of human parathyroid hormone (hPTH) or
PT hPTH-related protein -

XX

PS Claim 35; Fig 38; 56pp; English.

XX

CC The invention relates to a method for regulating proliferation or
CC enhancing differentiation of mammalian skin or hair cell. The method
CC involves administering nucleic acids encoding peptides derived from
CC N-terminal region of human parathyroid hormone (hPTH) or hPTH-related
CC peptide (PTHrP). The method is used for inhibiting hyperproliferative
CC skin disorders such as psoriasis, ichthyosis, eczema, acne, actinic
CC keratosis, skin cancer, for inhibiting hair growth or preventing hair
CC regrowth. It is useful for stimulating cell growth, rejuvenating aged
CC skin, preventing skin wrinkles, treating skin wrinkles, enhancing wound
CC healing, stimulating hair growth, maintaining hair growth, treating or
CC preventing female or male pattern baldness, for treating chemotherapy
CC induced alopecia and also for stimulating epidermal cell growth or
CC hair follicle cell growth. The method is also used in gene therapy.
CC The present sequence is hPTH peptide.

XX

SQ Sequence 28 AA;

Query Match 67.6%; Score 23; DB 23; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.9e-17;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||
Db 6 GKHLNSMERVEWLRKKLQDVHNF 28

RESULT 7

AAU73044

ID AAU73044 standard; Peptide; 28 AA.

XX

AC AAU73044;

XX

DT 12-MAR-2002 (first entry)

XX

DE Parathyroid hormone PTH/PTHrP modulating domain #26.

XX

KW Human; parathyroid hormone; PTH; parathyroid hormone-related protein;

KW PTHrP; bone resorption inhibitor; osteoprotegrin; OPG; OPG-L antibody;

KW calcitonin; bisphosphonate; oestrogen; oestrogen receptor; tibolone;

KW osteopenia; hyperthyroidism; hypercalcaemia; tumour metastasis; bone;

KW breast cancer; prostate cancer; cachexia; anorexia; osteoporosis;

KW Paget's disease; osteomyelitis; osteonecrosis; bone cell death;

KW Gaucher's disease; sickle cell anaemia; systemic lupus erythematosus;

KW rheumatoid arthritis; periodontal disease; alopecia; fracture repair;

KW immunoglobulin G; IgG.

XX

OS Homo sapiens.

XX

PN WO200181415-A2.

XX

PD 01-NOV-2001.

XX

PF 27-APR-2001; 2001WO-US13528.

XX

PR 27-APR-2000; 2000US-200053P.

PR 28-JUN-2000; 2000US-214860P.

PR 06-FEB-2001; 2001US-266673P.

PR 26-APR-2001; 2001US-0843221.

XX

PA (AMGE-) AMGEN INC.

XX

PI Kostenuik P, Liu C, Lacey DL;

XX

DR WPI; 2002-066435/09.

XX

PT Composition, useful for treating osteopenia, comprises parathyroid
PT hormone and parathyroid hormone-related protein receptor modulators -

XX

PS Disclosure; Page 27; 107pp; English.

XX

CC The invention relates to a composition (I) comprising modulators of
CC parathyroid hormone (PTH) and parathyroid hormone-related protein (PTHrP)
CC which comprise a PTH/PTHrP modulating domain and a vehicle. (I)

CC comprising PTH agonist optionally with a bone resorption inhibitor, such
 CC as osteoprotegerin (OPG), OPG-L antibody, calcitonin, bisphosphonates,
 CC oestrogens, oestrogen receptor modulators and tibolone is useful for
 CC treating osteopenia. (I) is useful for therapeutic and prophylactic
 CC purposes. Antagonists of PTH receptor are useful in treating primary and
 CC secondary hyperthyroidism, hypercalcaemia, tumour metastases,
 CC particularly breast and prostate cancer, cachexia and anorexia,
 CC osteopenia, including various forms of osteoporosis, Paget's disease of
 CC bone, osteomyelitis, osteonecrosis or bone cell death, associated with
 CC traumatic injury or nontraumatic necrosis associated with Gaucher's
 CC disease, sickle cell anaemia, systemic lupus erythematosus, rheumatoid
 CC arthritis, periodontal disease and alopecia. PTH receptor agonists are
 CC useful as therapeutic agents in conditions including fracture repair
 CC (including healing of non-union fractures), osteopenia, including various
 CC forms of osteoporosis. AAU73018-AAU73181 represent parathyroid hormone
 CC and parathyroid hormone related protein (PTH/PTHrP) modulators and
 CC related amino acid sequences of the invention.

XX

SQ Sequence 28 AA;

Query Match 67.6%; Score 23; DB 23; Length 28;
 Best Local Similarity 100.0%; Pred. No. 2.9e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 6 GKHLNSMERVEWLRKKLQDVHNF 28

RESULT 8

AAE23752

ID AAE23752 standard; peptide; 30 AA.

XX

AC AAE23752;

XX

DT 10-SEP-2002 (first entry)

XX

DE Human parathyroid hormone (hPTH) peptide (5-34).

XX

KW Human parathyroid hormone; hPTH; PTH-related peptide; PTHrP; eczema;
 KW hyperproliferative skin disorder; psoriasis; ichthyosis; skin cancer;
 KW acne; actinic keratosis; alopecia; gene therapy.

XX

OS Homo sapiens.

XX

PN WO200228420-A2.

XX

PD 11-APR-2002.

XX

PF 05-OCT-2001; 2001WO-US31082.

XX

PR 06-OCT-2000; 2000US-238134P.

XX

PA (HOLI/) HOLICK M F.

XX

PI Holick MF;

XX

DR WPI; 2002-452304/48.
 XX
 PT Regulating mammalian skin or hair cell proliferation and
 PT differentiation by administering nucleic acids encoding peptides
 PT derived from N-terminal region of human parathyroid hormone (hPTH) or
 PT hPTH-related protein -
 XX
 PS Claim 35; Fig 42; 56pp; English.
 XX
 CC The invention relates to a method for regulating proliferation or
 CC enhancing differentiation of mammalian skin or hair cell. The method
 CC involves administering nucleic acids encoding peptides derived from
 CC N-terminal region of human parathyroid hormone (hPTH) or hPTH-related
 CC peptide (PTHrP). The method is used for inhibiting hyperproliferative
 CC skin disorders such as psoriasis, ichthyosis, eczema, acne, actinic
 CC keratosis, skin cancer, for inhibiting hair growth or preventing hair
 CC regrowth. It is useful for stimulating cell growth, rejuvenating aged
 CC skin, preventing skin wrinkles, treating skin wrinkles, enhancing wound
 CC healing, stimulating hair growth, maintaining hair growth, treating or
 CC preventing female or male pattern baldness, for treating chemotherapy
 CC induced alopecia and also for stimulating epidermal cell growth or
 CC hair follicle cell growth. The method is also used in gene therapy.
 CC The present sequence is hPTH peptide.
 XX
 SQ Sequence 30 AA;

Query Match 67.6%; Score 23; DB 23; Length 30;
 Best Local Similarity 100.0%; Pred. No. 3.1e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 8 GKHLNSMERVEWLRKKLQDVHNF 30

RESULT 9

AAB07468
 ID AAB07468 standard; protein; 32 AA.
 XX
 AC AAB07468;
 XX
 DT 20-OCT-2000 (first entry)
 XX
 DE Antigenic peptide derived from human parathyroid hormone.
 XX
 KW Human; parathyroid hormone; PTH; hyperparathyroidism; bone disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200042437-A1.
 XX
 PD 20-JUL-2000.
 XX
 PF 13-JAN-2000; 2000WO-US00855.
 XX
 PR 14-JAN-1999; 99US-0231422.
 PR 26-JUN-1999; 99US-0344639.

XX
PA (SCAN-) SCANTIBODIES LAB INC.
XX
DR WPI; 2000-476147/41.
XX
PT Differentiating between normal parathyroid function and
PT hyperparathyroidism comprises determining and comparing whole
PT parathyroid hormone, parathyroid hormone inhibitory peptide fragment
PT and/or total parathyroid hormone levels -
XX
PS Disclosure; Page 6; 46pp; English.
XX
CC The present sequence represents an antigenic fragment derived from
CC human parathyroid hormone (PTH). It was used to raise antibodies.
CC PTH peptide fragments can function as PTH antagonists. The
CC specification describes a method for differentiating between a
CC person having substantially normal parathyroid function and having
CC hyperparathyroidism. The method comprises determining and comparing
CC at least two of the following parameters: whole parathyroid
CC hormone level, parathyroid hormone inhibitory peptide fragment level
CC and total parathyroid hormone level. The method is used for monitoring
CC (treatments of) parathyroid related bone disease and the effects of
CC therapeutic treatment for hyperparathyroidism.
XX
SQ Sequence 32 AA;

Query Match 67.6%; Score 23; DB 21; Length 32;
Best Local Similarity 100.0%; Pred. No. 3.2e-17;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||
Db 6 GKHLNSMERVEWLRKKLQDVHNF 28

RESULT 10

AAE23735

ID AAE23735 standard; peptide; 32 AA.

XX

AC AAE23735;

XX

DT 10-SEP-2002 (first entry)

XX

DE Human parathyroid hormone (hPTH) peptide (5-36).

XX

KW Human parathyroid hormone; hPTH; PTH-related peptide; PTHrP; eczema;
KW hyperproliferative skin disorder; psoriasis; ichthyosis; skin cancer;
KW acne; actinic keratosis; alopecia; gene therapy.

XX

OS Homo sapiens.

XX

PN WO200228420-A2.

XX

PD 11-APR-2002.

XX

PF 05-OCT-2001; 2001WO-US31082.

XX

PR 06-OCT-2000; 2000US-238134P.

XX

PA (HOLI/) HOLICK M F.

XX

PI Holick MF;

XX

DR WPI; 2002-452304/48.

DR N-PSDB; AAD37995.

XX

PT Regulating mammalian skin or hair cell proliferation and
PT differentiation by administering nucleic acids encoding peptides
PT derived from N-terminal region of human parathyroid hormone (hPTH) or
PT hPTH-related protein -

XX

PS Claim 35; Fig 40; 56pp; English.

XX

CC The invention relates to a method for regulating proliferation or
CC enhancing differentiation of mammalian skin or hair cell. The method
CC involves administering nucleic acids encoding peptides derived from
CC N-terminal region of human parathyroid hormone (hPTH) or hPTH-related
CC peptide (PTHrP). The method is used for inhibiting hyperproliferative
CC skin disorders such as psoriasis, ichthyosis, eczema, acne, actinic
CC keratosis, skin cancer, for inhibiting hair growth or preventing hair
CC regrowth. It is useful for stimulating cell growth, rejuvenating aged
CC skin, preventing skin wrinkles, treating skin wrinkles, enhancing wound
CC healing, stimulating hair growth, maintaining hair growth, treating or
CC preventing female or male pattern baldness, for treating chemotherapy
CC induced alopecia and also for stimulating epidermal cell growth or
CC hair follicle cell growth. The method is also used in gene therapy.
CC The present sequence is hPTH peptide.

XX

SQ Sequence 32 AA;

Query Match 67.6%; Score 23; DB 23; Length 32;

Best Local Similarity 100.0%; Pred. No. 3.2e-17;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34

|||||

Db 8 GKHLNSMERVEWLRKKLQDVHNF 30

RESULT 11

AAP30022

ID AAP30022 standard; peptide; 34 AA.

XX

AC AAP30022;

XX

DT 25-MAR-2003 (updated)

DT 01-SEP-1992 (first entry)

XX

DE Human parathyroid-(1-34) amide.

XX

KW PTH; parathyroid gland; antibodies.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers
 FT Modified-site 34
 FT /note= "amidated"
 XX
 PN JP58096052-A.
 XX
 PD 07-JUN-1983.
 XX
 PF 30-NOV-1983; 83JP-0193212.
 XX
 PR 31-MAR-1981; 81JP-0048887.
 XX
 PA (TOXN) TOYO JOZO KK.
 XX
 DR WPI; 1983-709291/28.
 XX
 PT High activity human parathyroid hormone amide prodn. - by
 PT condensing protected aminoacid(s) and/or peptide(s) useful for
 PT lowering parathyroid gland function
 XX
 PS Claim 1; Page 1; 20pp; Japanese.
 XX
 CC The human parathyroid hormone, hPTH(1-34)-amide was prepd. by
 CC the following steps: Firstly the carboxy gp. at the C-terminal
 CC phenylalanine was converted into its amide form. The protected
 CC individual amino acids were condensed, in order, by liquid phase
 CC synthesis. The protecting groups were removed from the N-terminal
 CC amino gp. and other functional gps. by acidolysis, and the
 CC resulting hPTH(1-34)-amide purified by gel filtration
 CC chromatography using a Sephadex G-25, G-50 or LH-20 column or by
 CC column chromatography with carboxymethyl cellulose or ion exchange
 CC resin. The peptide amide is useful in lowering the activity of the
 CC parathyroid gland and in the prepn. of antibodies for diagnosis of
 CC parathyroid gland function.
 CC (Updated on 25-MAR-2003 to correct PR field.)
 XX
 SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 4; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.4e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 12
 AAP50377

ID AAP50377 standard; peptide; 34 AA.
 XX
 AC AAP50377;
 XX
 DT 25-MAR-2003 (updated)
 DT 08-MAR-1992 (first entry)
 XX
 DE [Met(O)8,18]hPTH-(1-34).

XX
 KW Human parathyroid hormone; calcium regulation.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 8
 FT /label= oxidised methionine
 FT Modified-site 18
 FT /label= oxidised methionine
 XX
 PN JP59204159-A.
 XX
 PD 19-NOV-1984.
 XX
 PF 28-APR-1983; 83JP-0075607.
 XX
 PR 28-APR-1983; 83JP-0075607.
 XX
 PA (TOXN) TOYO JOZO KK.
 XX
 DR WPI; 1985-003560/01.
 XX
 PT New (Met(O)8,18)hPTH-(1-34) peptide - increases calcium level in
 PT blood and decreases level in urine.
 XX
 PS Claim 1; Page 1; 3pp; Japanese.
 XX
 CC Unmodified hPTH(1-34) increases Ca in blood, decreases P in blood,
 CC decreases Ca in urine and increases P in urine by increasing cAMP in
 CC urine and enhancing vitamin D hydroxylase activity in kidneys. The
 CC modified derivative only has the effect of lowering Ca levels in
 CC urine and can be used when only this particular effect is required.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 CC (Updated on 25-MAR-2003 to correct DR field.)
 XX
 SQ Sequence 34 AA;

 Query Match 67.6%; Score 23; DB 6; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.4e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 13

AAP60031

ID AAP60031 standard; peptide; 34 AA.

XX

AC AAP60031;

XX

DT 25-MAR-2003 (updated)

DT 06-JUL-1991 (first entry)

XX

DE Sequence of the first 34 AA residues of a parathyroid hormone

DE obtainable from a human or animal.
 XX
 KW Osteoporosis therapy.
 XX
 OS Homo sapiens/animal.
 XX
 PN EP197514-A.
 XX
 PD 15-OCT-1986.
 XX
 PF 03-APR-1986; 86EP-0104562.
 XX
 PR 04-APR-1985; 85US-0720018.
 PR 05-DEC-1986; 86US-0939308.
 PR 21-MAY-1987; 87US-0052383.
 XX
 PA (GEHO) GEN HOSPITAL CORP.
 XX
 PI Potts JT, Neer RM, Slovik DM;
 XX
 DR WPI; 1986-273437/42.
 XX
 PT Compsn. and kits for increasing bone mass in osteoporosis -
 PT contg. parathyroid hormone or fragment with hydroxylated
 PT vitamin/D cpd. or calcium salt
 XX
 PS Claim 4; Page 24; 26pp; English.
 XX
 CC The peptide is used in a pharmaceutical compsn. together with a
 CC hydroxylated vitamin D compound, or a non-toxic calcium salt, pref.
 CC CaCO3. The compsn. pref. contains 100-700 (pref. 200-600, esp. 400-
 CC 500) units of the peptide. The vitamin D compound is pref. 1-alpha-
 CC hydroxy vitamin D2 or 1-alpha,25-dihydroxy vitamin D2.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 7; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.4e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34
 ||||||||||||||||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 14

AAR07919

ID AAR07919 standard; protein; 34 AA.

XX

AC AAR07919;

XX

DT 18-FEB-1991 (first entry)

XX

DE Human parathyroid hormone analogue, hPTH(7-34).

XX

KW Osteoporosis; hypercalcemia; hyperparathyroidism; hypertension.

XX
 OS Homo sapiens.
 XX
 PN US4968669-A.
 XX
 PD 06-NOV-1990.
 XX
 PF 21-APR-1989; 89US-0341597.
 XX
 PR 21-APR-1989; 89US-0341597.
 PR 09-MAY-1988; 88US-0191512.
 XX
 PA (MERI) MERCK & CO INC.
 XX
 PI Rosenblatt M, Chorev M;
 XX
 DR WPI; 1990-354642/47.
 XX
 PT New parathyroid hormone analogues - which inhibit hormone
 PT activity by binding receptors while not producing second
 PT messenger molecules
 XX
 PS Claim 1; Column 8; 6pp; English.
 XX
 CC Peptide analogues have high affinity for PTH cell surface receptors,
 CC but do not stimulate production of secondary messenger molecules.
 CC They may be used in inhibition of PTH action, and in diagnosis and
 CC treatment of osteoporosis, hypercalcemia and hyperparathyroidism.
 CC Analogues may also be used in treatment of tumours and other cells
 CC overproducing peptide hormone-like substances, and immune diseases
 CC eg. allergic inflammation and hyperactive lymphocytes.
 CC Naturally occurring PTH levels may also be measured in vitro.
 XX
 SQ Sequence 34 AA;

 Query Match 67.6%; Score 23; DB 11; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.4e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 15

AAR22283

ID AAR22283 standard; peptide; 34 AA.
 XX
 AC AAR22283;
 XX
 DT 29-JUL-1992 (first entry)
 XX
 DE Parathyroid hormone analogue N-terminus [1-34].
 XX
 KW Human; hPTH; wound healing; hair growth; hyperproliferation skin;
 KW disorders; psoriasis; cancer; burns.
 XX

OS Homo sapiens.
 XX
 PN WO9204039-A.
 XX
 PD 19-MAR-1992.
 XX
 PF 30-AUG-1991; 91WO-US06218.
 XX
 PR 30-AUG-1990; 90US-0575219.
 XX
 PA (HOLI/) HOLICK M F.
 XX
 PI Holick MF;
 XX
 DR WPI; 1992-114063/14.
 XX
 PT Use of peptide having homology with parathyroid hormone - for
 PT enhancement of cell proliferation for wound healing
 XX
 PS Disclosure; Fig 1; 34pp; English.
 XX
 CC The peptide can be easily synthesised by recombinant DNA or solid
 CC phase peptide synthesis techniques. The peptide has > 50 percent
 CC homology with the N-terminal 1-34 amino acids of human parathyroid
 CC hormone or hypercalcaemic region. It is esp. PTH (7-34). The
 CC peptide may be used in a method for the treatment of hyperprolifer-
 CC ation skin disorders e.g. psoriasis, cancers, burns or skin
 CC ulcerations by inhibition of cell proliferation and enhancement of
 CC cell differentiation (agonist activity). They are also used to
 CC enhance cell proliferation (antagonist activity) for wound healing.
 CC They are also applicable in the promotion of new hair growth or
 CC stimulation of the rate of hair growth e.g. following chemotherapy
 CC or for treating alopecia e.g. male pattern baldness.
 XX
 SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 13; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.4e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 16

AAR22292

ID AAR22292 standard; Peptide; 34 AA.

XX

AC AAR22292;

XX

DT 25-MAR-2003 (updated)

DT 03-AUG-1992 (first entry)

XX

DE Human parathyroid hormone 1-34 [Phe 11].

XX

KW hPTH; protease resistant; osteoporosis; hypoparathyroidism;

KW hypertension.
 XX
 OS Synthetic.
 XX
 PN EP477885-A.
 XX
 PD 01-APR-1992.
 XX
 PF 25-SEP-1991; 91EP-0116303.
 XX
 PR 06-SEP-1991; 91JP-0227232.
 PR 28-SEP-1990; 90JP-0257490.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Nakagawa S, Fukuda T, Kawase M, Yamazaki I;
 XX
 DR WPI; 1992-106285/14.
 XX
 PT New peptide(s) are parathyroid hormone derivs. - used in hormone
 PT therapy, for treating osteoporosis hyperparathyroidism and
 PT hypertension
 XX
 PS Claim 9; Page 14; 14pp; English.
 XX
 CC The peptide is an analogue of human parathyroid hormone fragment
 CC 1-34. The peptide modification defined increase resistance to
 CC proteases and therefore persistence in the blood. The peptide is
 CC used in therapy of osteoporosis, hypoparathyroidism and hypertension.
 CC The peptide may be synthesised by the Merrifield solid phase
 CC method in an automatic apparatus.
 CC See also AAR22290-99.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 13; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.4e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 17

AAR22293

ID AAR22293 standard; Peptide; 34 AA.

XX

AC AAR22293;

XX

DT 25-MAR-2003 (updated)

DT 03-AUG-1992 (first entry)

XX

DE Human parathyroid hormone 1-34 [Leu 8].

XX

KW hPTH; protease resistant; osteoporosis; hypoparathyroidism;

KW hypertension.
 XX
 OS Synthetic.
 XX
 PN EP477885-A.
 XX
 PD 01-APR-1992.
 XX
 PF 25-SEP-1991; 91EP-0116303.
 XX
 PR 06-SEP-1991; 91JP-0227232.
 PR 28-SEP-1990; 90JP-0257490.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Nakagawa S, Fukuda T, Kawase M, Yamazaki I;
 XX
 DR WPI; 1992-106285/14.
 XX
 PT New peptide(s) are parathyroid hormone derivs. - used in hormone
 PT therapy, for treating osteoporosis hyperparathyroidism and
 PT hypertension
 XX
 PS Claim 9; Page 14; 14pp; English.
 XX
 CC The peptide is an analogue of human parathyroid hormone fragment
 CC 1-34. The peptide modification defined increase resistance to
 CC proteases and therefore persistence in the blood. The peptide is
 CC used in therapy of osteoporosis, hypoparathyroidism and hypertension.
 CC The peptide may be synthesised by the Merrifield solid phase
 CC method in an automatic apparatus.
 CC See also AAR22290-99.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 13; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.4e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 18

AAR22294

ID AAR22294 standard; Peptide; 34 AA.

XX

AC AAR22294;

XX

DT 25-MAR-2003 (updated)

DT 03-AUG-1992 (first entry)

XX

DE Human parathyroid hormone 1-34 [Ser 11].

XX

KW hPTH; protease resistant; osteoporosis; hypoparathyroidism;

KW hypertension.
 XX
 OS Synthetic.
 XX
 PN EP477885-A.
 XX
 PD 01-APR-1992.
 XX
 PF 25-SEP-1991; 91EP-0116303.
 XX
 PR 06-SEP-1991; 91JP-0227232.
 PR 28-SEP-1990; 90JP-0257490.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Nakagawa S, Fukuda T, Kawase M, Yamazaki I;
 XX
 DR WPI; 1992-106285/14.
 XX
 PT New peptide(s) are parathyroid hormone derivs. - used in hormone
 PT therapy, for treating osteoporosis hyperparathyroidism and
 PT hypertension
 XX
 PS Claim 9; Page 14; 14pp; English.
 XX
 CC The peptide is an analogue of human parathyroid hormone fragment
 CC 1-34. The peptide modification defined increase resistance to
 CC proteases and therefore persistence in the blood. The peptide is
 CC used in therapy of osteoporosis, hypoparathyroidism and hypertension.
 CC The peptide may be synthesised by the Merrifield solid phase
 CC method in an automatic apparatus.
 CC See also AAR22290-99.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 13; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.4e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 19

AAR22296

ID AAR22296 standard; Peptide; 34 AA.
 XX
 AC AAR22296;
 XX
 DT 25-MAR-2003 (updated)
 DT 03-AUG-1992 (first entry)
 XX
 DE Human parathyroid hormone 1-34 [Lys 11].
 XX
 KW hPTH; protease resistant; osteoporosis; hypoparathyroidism;

KW hypertension.
 XX
 OS Synthetic.
 XX
 PN EP477885-A.
 XX
 PD 01-APR-1992.
 XX
 PF 25-SEP-1991; 91EP-0116303.
 XX
 PR 06-SEP-1991; 91JP-0227232.
 PR 28-SEP-1990; 90JP-0257490.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Nakagawa S, Fukuda T, Kawase M, Yamazaki I;
 XX
 DR WPI; 1992-106285/14.
 XX
 PT New peptide(s) are parathyroid hormone derivs. - used in hormone
 PT therapy, for treating osteoporosis hyperparathyroidism and
 PT hypertension
 XX
 PS Claim 9; Page 14; 14pp; English.
 XX
 CC The peptide is an analogue of human parathyroid hormone fragment
 CC 1-34. The peptide modification defined increase resistance to
 CC proteases and therefore persistence in the blood. The peptide is
 CC used in therapy of osteoporosis, hypoparathyroidism and hypertension.
 CC The peptide may be synthesised by the Merrifield solid phase
 CC method in an automatic apparatus.
 CC See also AAR22290-99.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 13; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.4e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 20

AAR41549

ID AAR41549 standard; protein; 34 AA.

XX

AC AAR41549;

XX

DT 25-MAR-2003 (updated)

DT 11-APR-1994 (first entry)

XX

DE [D-Ser3]hPTH (1-34)NH2.

XX

KW PTH; parathyroid hormone; protease resistance; osteoporosis;

KW hypoparathyroidism; hypertension.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 3
 FT /note = "D-form residue"
 FT Modified-site 34
 FT /note = "C terminal is amidated"
 XX
 PN EP561412-A1.
 XX
 PD 22-SEP-1993.
 XX
 PF 18-MAR-1993; 93EP-0104500.
 XX
 PR 19-MAR-1992; 92JP-0063517.
 PR 18-FEB-1993; 93JP-0029283.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Fukuda T, Nakagawa S, Taketomi S;
 XX
 DR WPI; 1993-296712/38.
 XX
 PT New parathyroid hormone derivs. - used for the treatment of
 PT osteoporosis hypoparathyroidism and hypertension
 XX
 PS Example 1; Page 17; 37pp; English.
 XX
 CC Human parathyroid hormone (PTH) analogues (AAR41548 - generic sequence;
 CC AAR41549-R41582 - specific examples) show increased resistance to
 CC proteases and a greater persistency of activity within the blood is
 CC obtained. The proteins can be used to treat a number of bone and blood
 CC disorders. This analogue was used as a test compound.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 14; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.4e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 21

AAR41550

ID AAR41550 standard; protein; 34 AA.

XX

AC AAR41550;

XX

DT 25-MAR-2003 (updated)

DT 11-APR-1994 (first entry)

XX

DE [D-Ala3]hPTH (1-34).
 XX
 KW PTH; parathyroid hormone; protease resistance; osteoporosis;
 KW hypoparathyroidism; hypertension.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 3
 FT /note = "D-form residue"
 XX
 PN EP561412-A1.
 XX
 PD 22-SEP-1993.
 XX
 PF 18-MAR-1993; 93EP-0104500.
 XX
 PR 19-MAR-1992; 92JP-0063517.
 PR 18-FEB-1993; 93JP-0029283.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Fukuda T, Nakagawa S, Taketomi S;
 XX
 DR WPI; 1993-296712/38.
 XX
 PT New parathyroid hormone derivs. - used for the treatment of
 PT osteoporosis hypoparathyroidism and hypertension
 XX
 PS Example 1; Page 17; 37pp; English.
 XX
 CC Human parathyroid hormone (PTH) analogues (AAR41548 - generic sequence;
 CC AAR41549-R41582 - specific examples) show increased resistance to
 CC proteases and a greater persistency of activity within the blood is
 CC obtained. The proteins can be used to treat a number of bone and blood
 CC disorders. This analogue has a relative biological activity to hPTH(1-34)
 CC of 2.17.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 14; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.4e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 22

AAR41570

ID AAR41570 standard; protein; 34 AA.

XX

AC AAR41570;

XX

DT 25-MAR-2003 (updated)

DT 11-APR-1994 (first entry)
 XX
 DE [Gln25]hPTH (1-34).
 XX
 KW PTH; parathyroid hormone; protease resistance; osteoporosis;
 KW hypoparathyroidism; hypertension.
 XX
 OS Homo sapiens.
 XX
 PN EP561412-A1.
 XX
 PD 22-SEP-1993.
 XX
 PF 18-MAR-1993; 93EP-0104500.
 XX
 PR 19-MAR-1992; 92JP-0063517.
 PR 18-FEB-1993; 93JP-0029283.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Fukuda T, Nakagawa S, Taketomi S;
 XX
 DR WPI; 1993-296712/38.
 XX
 PT New parathyroid hormone derivs. - used for the treatment of
 PT osteoporosis hypoparathyroidism and hypertension
 XX
 PS Example 1; Page 27; 37pp; English.
 XX
 CC Human parathyroid hormone (PTH) analogues (AAR41548 - generic sequence;
 CC AAR41549-R41582 - specific examples) show increased resistance to
 CC proteases and a greater persistency of activity within the blood is
 CC obtained. The proteins can be used to treat a number of bone and blood
 CC disorders. This analogue was used as a test compound.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 14; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.4e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 23

AAR49697

ID AAR49697 standard; Protein; 34 AA.

XX

AC AAR49697;

XX

DT 14-SEP-1994 (first entry)

XX

DE Sequence of variant of human parathyroid hormone [Ala8]hPTH(1-34).

XX

KW Parathyroid hormone; bone-stimulating; non-vasoactive compound;
 KW osteoporosis; therapy.
 XX
 OS Synthetic.
 XX
 PN CA2098639-A.
 XX
 PD 20-DEC-1993.
 XX
 PF 17-JUN-1993; 93CA-2098639.
 XX
 PR 19-JUN-1992; 92US-0900680.
 XX
 PA (ALLX) ALLELIX BIOPHARMACEUTICALS INC.
 PA (GLAX) GLAXO CANADA INC.
 XX
 PI Bozzato RP, Kronis KA;
 XX
 DR WPI; 1994-074853/10.
 XX
 PT New Met8-substd. variants of parathyroid hormone - stimulate bone
 PT and are non-vasoactive, useful for treating, e.g. osteoporosis
 XX
 PS Claim 13; Fig 2; 31pp; English.
 XX
 CC AAQ58564 is the sequence of wild-type human parathyroid hormone. In
 CC the cpds of the invention, Met 8 is replaced with Cys, Val or Ala.
 CC In addition, Met 18 may be replaced with Leu. Moreover truncated
 CC variants of 34 AAs with Ala or Cys substituted for Met 8 are also
 CC claimed. The variants have reduced vasoactivity relative to Met 8-
 CC contg. hPTH and are useful for the treatment of bone disorders, such
 CC as osteoporosis. Dosage is 1 microgram - 100 milligram (pref. 1-
 CC microgram - 1000 microgram)/kg.
 XX
 SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 15; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.4e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 24

AAR49698

ID AAR49698 standard; Protein; 34 AA.

XX

AC AAR49698;

XX

DT 14-SEP-1994 (first entry)

XX

DE Sequence of variant of human parathyroid hormone [Cys8]hPTH(1-34).

XX

KW Parathyroid hormone; bone-stimulating; non-vasoactive compound;
 KW osteoporosis; therapy.

XX
 OS Synthetic.
 XX
 PN CA2098639-A.
 XX
 PD 20-DEC-1993.
 XX
 PF 17-JUN-1993; 93CA-2098639.
 XX
 PR 19-JUN-1992; 92US-0900680.
 XX
 PA (ALLX) ALLELIX BIOPHARMACEUTICALS INC.
 PA (GLAX) GLAXO CANADA INC.
 XX
 PI Bozzato RP, Kronis KA;
 XX
 DR WPI; 1994-074853/10.
 XX
 PT New Met8-substd. variants of parathyroid hormone - stimulate bone
 PT and are non-vasoactive, useful for treating, e.g. osteoporosis
 XX
 PS Claim 14; Fig 2; 31pp; English.
 XX
 CC AAQ58564 is the sequence of wild-type human parathyroid hormone. In
 CC the cpds of the invention, Met 8 is replaced with Cys, Val or Ala.
 CC In addition, Met 18 may be replaced with Leu. Moreover truncated
 CC variants of 34 AAs with Ala or Cys substituted for Met 8 are also
 CC claimed. The variants have reduced vasoactivity relative to Met 8-
 CC contg. hPTH and are useful for the treatment of bone disorders, such
 CC as osteoporosis. Dosage is 1 microgram - 100 milligram (pref. 1-
 CC microgram - 1000 microgram)/kg.
 XX
 SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 15; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.4e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 25

AAR58291

ID AAR58291 standard; peptide; 34 AA.

XX

AC AAR58291;

XX

DT 20-SEP-1994. (first entry)

XX

DE [Lys(For)26, Lys(For)27]-hPTH(1-34)-NH2.

XX

KW Human parathyroid hormone; hPTH; variant; analogue;

KW calcium; depletion; fixation; resorption; osteopathy; osteoporosis;

KW hypoparathyroidism.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 26

FT /label= Other

FT /note= "Formyl-Lys."

FT Modified-site 27

FT /label= Other

FT /note= "Formyl-Lys."

FT Modified-site 34

FT /note= "in amide form"

XX

PN GB2269176-A.

XX

PD 02-FEB-1994.

XX

PF 12-JUL-1993; 93GB-0014384.

XX

PR 15-JUL-1992; 92GB-0015009.

PR 18-DEC-1992; 92GB-0026415.

PR 23-DEC-1992; 92GB-0026859.

PR 23-DEC-1992; 92GB-0026861.

PR 28-JAN-1993; 93GB-0001691.

PR 28-JAN-1993; 93GB-0001692.

PR 14-APR-1993; 93GB-0007673.

PR 19-APR-1993; 93GB-0008033.

XX

PA (SANO) SANDOZ LTD.

PA (BAUE/) BAUER W.

PA (SANO) SANDOZ PATENT GMBH.

PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.

XX

PI Albert R, Bauer W, Breckenridge R, Cardinaux F;

PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H;

PI Waelchli R, Rainer A;

XX

DR WPI; 1994-018352/03.

XX

PT New active para-thyroid hormone variants - used for treating or
PT preventing osteoporosis etc.

XX

PS Example 289; Page 47; 92pp; English.

XX

CC This peptide is an example of a highly generic formula covering
CC parathyroid hormone variants useful for treating or preventing bone
CC conditions associated with calcium depletion/resorption, in cases
CC where calcium fixation is required (esp. osteoporosis) or to treat
CC hypoparathyroidism.

XX

SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 15; Length 34;

Best Local Similarity 100.0%; Pred. No. 3.4e-17;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34

|||||||

Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 26

AAR58228

ID AAR58228 standard; peptide; 34 AA.

XX

AC AAR58228;

XX

DT 20-SEP-1994 (first entry)

XX

DE [D-Asp30]-hPTH(1-34)-NH2.

XX

KW Human parathyroid hormone; hPTH; variant; analogue;
KW calcium; depletion; fixation; resorption; osteopathy; osteoporosis;
KW hypoparathyroidism.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 30

FT /note= "D-form residue."

FT Modified-site 34

FT /note= "in amide form"

XX

PN GB2269176-A.

XX

PD 02-FEB-1994.

XX

PF 12-JUL-1993; 93GB-0014384.

XX

PR 15-JUL-1992; 92GB-0015009.

PR 18-DEC-1992; 92GB-0026415.

PR 23-DEC-1992; 92GB-0026859.

PR 23-DEC-1992; 92GB-0026861.

PR 28-JAN-1993; 93GB-0001691.

PR 28-JAN-1993; 93GB-0001692.

PR 14-APR-1993; 93GB-0007673.

PR 19-APR-1993; 93GB-0008033.

XX

PA (SANO) SANDOZ LTD.

PA (BAUE/) BAUER W.

PA (SANO) SANDOZ PATENT GMBH.

PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.

XX

PI Albert R, Bauer W, Breckenridge R, Cardinaux F;
PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H;
PI Waelchli R, Rainer A;

XX

DR WPI; 1994-018352/03.

XX

PT New active para-thyroid hormone variants - used for treating or
PT preventing osteoporosis etc.

XX

PS Example 226; Page 45; 92pp; English.

XX

CC This peptide is an example of a highly generic formula covering

XX
 PI Albert R, Bauer W, Breckenridge R, Cardinaux F;
 PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H;
 PI Waelchli R, Rainer A;
 XX
 DR WPI; 1994-018352/03.
 XX
 PT New active para-thyroid hormone variants - used for treating or
 PT preventing osteoporosis etc.
 XX
 PS Example 1; Page 30; 92pp; English.
 XX
 CC This peptide is an example of a highly generic formula covering
 CC parathyroid hormone variants useful for treating or preventing bone
 CC conditions associated with calcium depletion/resorption, in cases
 CC where calcium fixation is required (esp. osteoporosis) or to treat
 CC hypoparathyroidism.
 XX
 SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 15; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.4e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 28

AAR58017

ID AAR58017 standard; peptide; 34 AA.

XX

AC AAR58017;

XX

DT 20-SEP-1994 (first entry)

XX

DE [Lys(N-epsilon-Isopropyl)26,27]-human parathyroid hormone(1-34)-NH2.

XX

KW Human parathyroid hormone; hPTH; variant; analogue;
 KW calcium; depletion; fixation; resorption; osteopathy; osteoporosis;
 KW hypoparathyroidism.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 26

FT /note= "N-epsilon-Isopropyl-Lys"

FT Modified-site 27

FT /note= "N-epsilon-Isopropyl-Lys"

FT Modified-site 34

FT /note= "in amide form"

XX

PN GB2269176-A.

XX

PD 02-FEB-1994.

XX

PF 12-JUL-1993; 93GB-0014384.

XX

PR 15-JUL-1992; 92GB-0015009.

PR 18-DEC-1992; 92GB-0026415.

PR 23-DEC-1992; 92GB-0026859.

PR 23-DEC-1992; 92GB-0026861.

PR 28-JAN-1993; 93GB-0001691.

PR 28-JAN-1993; 93GB-0001692.

PR 14-APR-1993; 93GB-0007673.

PR 19-APR-1993; 93GB-0008033.

XX

PA (SANO) SANDOZ LTD.

PA (BAUE/) BAUER W.

PA (SANO) SANDOZ PATENT GMBH.

PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.

XX

PI Albert R, Bauer W, Breckenridge R, Cardinaux F;

PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H;

PI Waelchli R, Rainer A;

XX

DR WPI; 1994-018352/03.

XX

PT New active para-thyroid hormone variants - used for treating or
PT preventing osteoporosis etc.

XX

PS Example 2; Page 32; 92pp; English.

XX

CC This peptide is an example of a highly generic formula covering
CC parathyroid hormone variants useful for treating or preventing bone
CC conditions associated with calcium depletion/resorption, in cases
CC where calcium fixation is required (esp. osteoporosis) or to treat
CC hypoparathyroidism.

XX

SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 15; Length 34;

Best Local Similarity 100.0%; Pred. No. 3.4e-17;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34

|||||

Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 29

AAR55724

ID AAR55724 standard; peptide; 34 AA.

XX

AC AAR55724;

XX

DT 25-MAR-2003 (updated)

DT 16-NOV-1994 (first entry)

XX

DE Parathormone N-terminal sequence.

XX

KW Parathormone; parathyroid hormone; fatty acyl-peptide; conjugate;
KW antiproliferative; tumor; psoriasis; docosaheanoic acid; DHA;

KW eicosapentaenoic acid; EPA; antitumor.
 XX
 OS Synthetic.
 XX
 PN WO9412530-A1.
 XX
 PD 09-JUN-1994.
 XX
 PF 29-NOV-1993; 93WO-HU00065.
 XX
 PR 30-NOV-1992; 92US-0984293.
 XX
 PA (BIOS-) BIOSIGNAL KUTATO FEJLESZTO KFT.
 PA (SYNT-) SYNTHETIC PEPTIDES INC.
 XX
 PI Balogh A, Cachia PJ, Hodges RS, Horvath A, Keri G;
 PI Szederkenyi F, Vadasz Z;
 XX
 DR WPI; 1994-200194/24.
 XX
 PT New fatty acyl-peptide conjugates for inhibiting cell
 PT proliferation - more active than free peptide, partic. for
 PT treating tumours, virus-infected cells, psoriasis, etc.
 XX
 PS Disclosure; Fig. 1; 45pp; English.
 XX
 CC The peptides given in AAR55718-48 can each be conjugated through an
 CC amide linkage with a polyunsaturated fatty acid moiety, such as
 CC docosahexaenoic acid (DHA) or eicosapentanoic acid, to improve
 CC antiproliferative activity. The parathormone N-terminal fragment
 CC inhibits osteoblast proliferation.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 15; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.4e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 30

AAR74521

ID AAR74521 standard; Peptide; 34 AA.

XX

AC AAR74521;

XX

DT 25-MAR-2003 (updated)

DT 04-DEC-1995 (first entry)

XX

DE Human parathyroid hormone (1-34).

XX

KW Analogue; truncated human parathyroid hormone; PTH; hPTH; substitution;
 KW osteoporosis; hypercalcaemia; hyperparathroidism;

KW metabolic bone disease; human; veterinary medicine;
 KW iontophoretic transdermal transport; recombinant E.coli.
 XX
 OS Homo sapiens.
 XX
 PN WO9511988-A1.
 XX
 PD 04-MAY-1995.
 XX
 PF 25-OCT-1994; 94WO-US12205.
 XX
 PR 25-OCT-1993; 93US-0142551.
 XX
 PA (AFFY-) AFFYMAX TECHNOLOGIES NV.
 XX
 PI Oldenburg KR, Selick HE;
 XX
 DR WPI; 1995-178880/23.
 XX
 PT New active analogues of parathyroid hormone - with increased
 PT activity, stability in serum etc., esp. for treating
 PT osteoporosis, also related DNA and vectors
 XX
 PS Disclosure; Page 1; 109pp; English.
 XX
 CC This sequence represents residues 1-34 of human parathyroid hormone
 CC (RPTH). This sequence was used in the production of analogues of the
 CC truncated form of PTH. These analogues have increased activity and
 CC longer serum half life than native PTH due to eg. substitution of Met
 CC residues with Leu residues and replacing the carboxy Phe with Tyr. The
 CC carboxy terminal may also be modified by the addition of a homoserine
 CC residue or analogue, or by the addition of residues 35-84 of wild type
 CC PTH (see AAR74410). These PTH analogues may be used in the treatment of
 CC osteoporosis or hypercalcaemia, hyperparathroidism or other metabolic
 CC bone diseases in human or veterinary medicine. These peptides may also
 CC have increased iontophoretic transdermal transport compared to wild type
 CC PTH and can be produced in high yield in recombinant E.coli.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 16; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.4e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
 ||||||||||||||||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 31
 AAW99449
 ID AAW99449 standard; peptide; 34 AA.
 XX
 AC AAW99449;
 XX
 DT 08-JUN-1999 (first entry)

XX
 DE Human parathyroid hormone aal-34.
 XX
 KW Parathyroid hormone; PTH; parathormone; premature birth; pregnancy;
 KW spontaneous abortion; uterine contraction; human.
 XX
 OS Homo sapiens.
 XX
 PN US5880093-A.
 XX
 PD 09-MAR-1999.
 XX
 PF 05-APR-1995; 95US-0411726.
 XX
 PR 28-SEP-1992; 92IT-MI02331.
 XX
 PA (BAGN/) BAGNOLI F.
 XX
 PI Bagnoli F;
 XX
 DR WPI; 1996-162392/17.
 XX
 PT Use of composition containing parathormone or fragments - for
 PT preventing premature birth or spontaneous abortion or for treating
 PT unwanted uterine contractions
 XX
 PS Disclosure; Column 7-8; 11pp; English.
 XX
 CC Peptides AAW99448-W99452 represent all or part of the parathyroid
 CC hormone (PTH; parathormone) sequence or related peptide. The peptides
 CC are used for preventing premature birth, spontaneous abortion or unwanted
 CC uterine contractions in a pregnant human patient.
 CC (Note: this patent is the first Major Country Equivalent to Italian
 CC Patent IT1255388).
 XX
 SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 17; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.4e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 32

AAW15812

ID AAW15812 standard; peptide; 34 AA.

XX

AC AAW15812;

XX

DT 25-MAR-2003 (updated)

DT 05-JUN-1997 (first entry)

XX

DE [Trp(10)]-hPTH(1-34)-OH.

XX

KW human parathyroid hormone; human parathyroid hormone related peptide;
KW hPTH; hPTHrP; antagonist; hyperparathyroidism; hypercalcaemia;
KW tumour; dermatological disorders; hair growth promoter.
XX
OS Synthetic.
XX
PN WO9603437-A1.
XX
PD 08-FEB-1996.
XX
PF 27-JUL-1995; 95WO-EP02993.
XX
PR 28-JUL-1994; 94GB-0015255.
PR 28-JUL-1994; 94GB-0015254.
XX
PA (SANO) SANDOZ LTD.
PA (SANO) SANDOZ PATENT GMBH.
PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
XX
PI Cardinaux F, Feyen JHM, Gamse R, Gombert FO;
XX
DR WPI; 1996-117003/12.
XX
PT New parathyroid hormone or parathyroid hormone related peptide cpds.
PT - useful for preventing or treating conditions associated with
PT increased plasma calcium, tumour growth and dermatological disorders
XX
PS Example 9; Page 9; 32pp; English.
XX
CC New parathyroid hormone (PTH) or parathyroid hormone related peptide
CC (PTHrP) compounds are claimed in which (i) at least one of the amino
CC acid residues naturally occurring in positions 2 and 10 is replaced
CC by tryptophan or another amino acid residue bearing an aromatic or
CC heteroaromatic group on its side chain, and (ii) optionally at least
CC one of the amino acid residues naturally occurring in positions 3 and 6
CC is further replaced by tryptophan or another amino acid residue bearing
CC an aromatic or heteroaromatic group on its side chain. The peptides are
CC PTH or PTHrP antagonists useful for preventing or treating conditions
CC associated with increased plasma calcium caused by excessive release of
CC PTH or PTHrP (e.g. hyperparathyroidism, or hypercalcemia associated with
CC malignancy); for preventing or treating tumour growth stimulated by
CC PTHrP; for treating dermatological disorders; and for promoting hair
CC growth. They may be used in combination with a further active agent,
CC e.g. a bone resorption inhibitor or cytostatic agent.
CC The present sequence is a specific example of the new peptides.
CC (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 17; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-17;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 33

AAR99978

ID AAR99978 standard; peptide; 34 AA.

XX

AC AAR99978;

XX

DT 30-APR-1997 (first entry)

XX

DE Human parathyroid hormone peptide fragment (1-34).

XX

KW cyclic parathyroid hormone fragment; calcium-regulating activity;

KW osteoporosis; inhibit proliferation; epidermal cell; psoriasis;

KW improved half life; calcium retention; bone.

XX

OS Synthetic.

XX

PN DE19508672-A1.

XX

PD 12-SEP-1996.

XX

PF 10-MAR-1995; 95DE-1008672.

XX

PR 10-MAR-1995; 95DE-1008672.

XX

PA (BOEF) BOEHRINGER MANNHEIM GMBH.

XX

PI Dony C, Esswein A, Hoffmann E, Honold K, Schaefer W;

XX

DR WPI; 1996-413519/42.

XX

PT Cyclic parathyroid hormone fragments with lactam bridge - have good

PT in vivo half life and are useful for treating osteoporosis and

PT preventing epidermal cell proliferation

XX

PS Disclosure; Page 9; 14pp; German.

XX

CC New cyclic parathyroid hormone fragments (CPTH) have the amino acid
 CC sequence of h, b, p, r or CPTH(1-34), opt. extended by up to 4 amino
 CC acids (aa) at the C-terminus and opt. shortened by up to 3 amino acids at
 CC the N-terminus, and are cyclised between positions 13 and 17. One of
 CC these positions is occupied by L- or D- Orn or Lys, and the other by L-
 CC or D- Glu or Asp. CPTH have calcium-regulating activity (esp. for
 CC treating osteoporosis and inhibit proliferation of epidermal cells (for
 CC treating psoriasis). The CPTH have an improved half life in vivo than
 CC known PTH fragments, increased mitogenicity and DNA-synthesising
 CC capacity, reduced catabolic, calcium-mobilising activity and increased
 CC activity for calcium retention and incorporation into bone. The
 CC present sequence is that of human PTH peptide fragment (1-34).

XX

SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 17; Length 34;

Best Local Similarity 100.0%; Pred. No. 3.4e-17;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34

Db |||||
12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 34

AAR98951

ID AAR98951 standard; peptide; 34 AA.

XX

AC AAR98951;

XX

DT 15-JAN-1997 (first entry)

XX

DE Target peptide (PTH(1-34)) used in fusion protein construct.

XX

KW Fusion protein construct; isolation; purification;
KW growth hormone releasing factor; glucagon-like peptide 1;
KW parathyroid hormone; inclusion body; carbonic anhydrase.

XX

OS Synthetic.

XX

PN WO9617942-A1.

XX

PD 13-JUN-1996.

XX

PF 07-DEC-1995; 95WO-US15800.

XX

PR 07-DEC-1994; 94US-0350530.

XX

PA (BION-) BIONEBRASKA INC.

XX

PI De LA MOTTE RS, Henriksen DB, Holmquist B, Manning SD;

PI Partridge BE, Stout JS, Wagner FW;

XX

DR WPI; 1996-287186/29.

XX

PT Isolation and purificn of peptide(s) from fusion protein constructs
PT - which include a carbonic anhydrase and a variable fused
PT polypeptide

XX

PS Claim 18; Page 48; 67pp; English.

XX

CC A new method for the isolation and/or purification of a recombinant
CC peptide employs a fusion protein construct (FPC) comprising a
CC carbonic anhydrase and a variable fused polypeptide containing a
CC target peptide. The method comprises precipitating either the FPC or
CC a fragment of the FPC including the carbonic anhydrase. An
CC alternative method of producing the peptide comprises expressing the
CC FPC as part of an inclusion body. The target peptides of the FPC are
CC derived from growth hormone releasing factor (GRF), glucagon-like
CC peptide 1 (GLP1) or parathyroid hormone (PTH). This sequence
CC corresponds to amino acids 1-34 of PTH.

XX

SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 17; Length 34;

Best Local Similarity 100.0%; Pred. No. 3.4e-17;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
| | | | | | | | | | | | | | | | | |
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 35

AAR98966

ID AAR98966 standard; Peptide; 34 AA.

XX

AC AAR98966;

XX

DT 02-DEC-1996 (first entry)

XX

DE PTH(1-34).

XX

KW PTH; parathyroid hormone; parathormone; C-amide;

KW C-amidated peptide; alpha-carboxamide; recombinant protein;

KW fusion protein; transpeptidation.

XX

OS Not specified.

XX

PN WO9617941-A2.

XX

PD 13-JUN-1996.

XX

PF 07-DEC-1995; 95WO-US15799.

XX

PR 07-DEC-1994; 94US-0350528.

XX

PA (BION-) BIONEBRASKA INC.

XX

PI Heriksen DB, Holmquist B, Patridge BE, Stout JS;

PI Wagner FW;

XX

DR WPI; 1996-287185/29.

XX

PT Production of C-terminal alpha-carboxamidated peptide(s) - by

PT cleavage and transpeptidation of recombinant multicopy peptide(s) or

PT fusion constructs

XX

PS Claim 12; Page 70; 93pp; English.

XX

CC GLP1(7-35), GRF(1-44) and PTH(1-34) peptides (AAR98964-66) can be

CC produced as C-terminal amidated peptides utilising novel recombinant

CC protein constructs (see also AAR98967-72) in which single or multiple

CC copies of the peptide are linked by intraconnecting peptides that

CC permit the construct to be selectively reacted to produce product

CC peptides having a C-terminal alpha-carboxamide. Expression cassettes

CC (see also AAT34865-70) can be incorporated into vectors allowing prodn.

CC of the recombinant proteins in transformed E. coli host cells.

XX

SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 17; Length 34;

Best Local Similarity 100.0%; Pred. No. 3.4e-17;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34
| | | | | | | | | | | | | | | | | |
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 36

AAR88835

ID AAR88835 standard; peptide; 34 AA.

XX

AC AAR88835;

XX

DT 07-OCT-1996 (first entry)

XX

DE Human parathyroid hormone analogue, cyclo-PTH(1-34)-NH2.

XX

KW Parathyroid hormone; PTH; analogue; osteoporosis; bone cell;

KW calcium regulation; reduced PKC activity; protein kinase C;

KW increased adenylyl cyclase activity; cAMPase; cyclic; bone loss.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 10

FT /note= "forms peptide bond with Lys at posn. 26"

FT Modified-site 14

FT /note= "forms peptide bond with Asp at posn. 30"

FT Modified-site 26

FT /note= "forms peptide bond with Asn at posn. 10"

FT Modified-site 30

FT /note= "forms peptide bond with His at posn. 14"

FT Modified-site 34

FT /note= "amidated"

XX

PN CA2126299-A.

XX

PD 21-DEC-1995.

XX

PF 20-JUN-1994; 94CA-2126299.

XX

PR 20-JUN-1994; 94CA-2126299.

XX

PA (WILL/) WILICK G E.

XX

PI Neugebauer W, Sung WL, Surewicz W, Whitfield JF;

PI Willick GE;

XX

DR WPI; 1996-151754/16.

XX

PT New human parathyroid hormone analogues - which have increased

PT adenylyl cyclase activating activity, used for treating osteoporosis

XX

PS Claim 3; Fig 8; 21pp; English.

XX

CC AAR88829-R88841 are human parathyroid hormone (hPTH) analogues. The

CC analogues increase G-protein coupled adenylyl cyclase (cAMPase)

CC activity and reduce protein kinase C (PKC) activity. The analogues

CC can reverse the loss of bone and increase bone mass and density
CC without undesirable effects. They are useful for the treatment of
CC osteoporosis and other bone related disorders and disorders
CC involving bone cell calcium regulation.

XX
SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 17; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-17;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 37

AAW24273

ID AAW24273 standard; protein; 34 AA.

XX
AC AAW24273;

XX
DT 17-OCT-1997 (first entry)

XX
DE Wild type parathyroid hormone.

XX
KW Analogue; parathyroid hormone; PTH; hirudin; hirulog;
KW electrotransportability; alpha-helix; beta-sheet.

XX
OS Homo sapiens.

XX
PN WO9639423-A2.

XX
PD 12-DEC-1996.

XX
PF 06-JUN-1996; 96WO-US09647.

XX
PR 06-JUN-1995; 95US-0468275.

XX
PA (ALZA) ALZA CORP.

XX
PI Holladay LA, Oldenburg KR;

XX
DR WPI; 1997-043058/04.

XX
PT Prepn. of analogues of parent poly-peptide(s), esp. parathyroid
PT hormone and hirulog - which exhibit better or enhanced
PT electro-transportability through a body surface

XX
PS Claim 7; Fig 1A; 55pp; English.

XX
CC The sequences given in AAW24273-76 represent wildtype and analogues of
CC parathyroid hormone (PTH). The analogues exhibit better/enhanced
CC electrotransportability through a body surface, and are characterised
CC by substituting one or more amino acid residues of the parent
CC polypeptide to disrupt one or more alpha-helical and/or beta-sheet
CC segments of the parent polypeptide. An electrotransport device can

CC deliver the polypeptide analogue through a body surface by electro-
CC transport by including providing a therapeutically effective amount
CC of the polypeptide analogue in a donor reservoir of the electrotransport
CC device. The electrotransport flux of a polypeptide is increased by
CC reducing the potential of the polypeptide for forming alpha-helix or
CC beta-sheet segment.

XX

SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 18; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-17;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
| | | | | | | | | | | | | | | | | | | | | |
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 38

AAW08120

ID AAW08120 standard; peptide; 34 AA.

XX

AC AAW08120;

XX

DT 10-OCT-1997 (first entry)

XX

DE Human PTH derivative, [Aad10]hPTH(1-34).

XX

KW Human; parathyroid hormone; PTH; cAMP-producing activity;
KW bone formation; osteoporosis; hypoparathyroidism; hypertension;
KW climacteric disturbance.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 10

FT /label= Aad

XX

PN EP748817-A2.

XX

PD 18-DEC-1996.

XX

PF 13-JUN-1996; 96EP-0109475.

XX

PR 15-JUN-1995; 95JP-0148652.

XX

PA (TAKE) TAKEDA CHEM IND LTD.

XX

PI Fukuda T, Habashita J, Nakagawa S, Taketomi S;

XX

DR WPI; 1997-036114/04.

XX

PT New parathyroid hormone derivs. - useful in treatment of bone
PT diseases, hypoparathyroidism and hypertension

XX

PS Example 1; Page 29; 42pp; English.

XX

CC The sequences given in AAW08108-32 represent derivatives of human
CC parathyroid hormone (PTH). These peptides are human PTH (1-34)
CC derivative peptides. They have potent cAMP-producing activity and
CC bone formation activity. They may be used in treatment of bone
CC diseases including osteoporosis, hypoparathyroidism, hypertension
CC and climacteric disturbance. The peptides are low in toxicity and
CC are safe.

XX

SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 18; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-17;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
| | | | | | | | | | | | | | | | | |
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 39

AAW08108

ID AAW08108 standard; peptide; 34 AA.

XX

AC AAW08108;

XX

DT 10-OCT-1997 (first entry)

XX

DE Human parathyroid hormone derivative, [Asp10,Lys11]hPTH(1-34).

XX

KW Human; parathyroid hormone; PTH; cAMP-producing activity;

KW bone formation; osteoporosis; hypoparathyroidism; hypertension;

KW climacteric disturbance.

XX

OS Synthetic.

XX

PN EP748817-A2.

XX

PD 18-DEC-1996.

XX

PF 13-JUN-1996; 96EP-0109475.

XX

PR 15-JUN-1995; 95JP-0148652.

XX

PA (TAKE) TAKEDA CHEM IND LTD.

XX

PI Fukuda T, Habashita J, Nakagawa S, Taketomi S;

XX

DR WPI; 1997-036114/04.

XX

PT New parathyroid hormone derivs. - useful in treatment of bone
PT diseases, hypoparathyroidism and hypertension

XX

PS Claim 27; Page 26; 42pp; English.

XX

CC The sequences given in AAW08108-32 represent derivatives of human
CC parathyroid hormone (PTH). These peptides are human PTH (1-34)
CC derivative peptides. They have potent cAMP-producing activity and

CC bone formation activity. They may be used in treatment of bone
CC diseases including osteoporosis, hypoparathyroidism, hypertension
CC and climacteric disturbance. The peptides are low in toxicity and
CC are safe.

XX

SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 18; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-17;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
| | | | | | | | | | | | | | | | | | | | | |
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 40

AAW08109

ID AAW08109 standard; peptide; 34 AA.

XX

AC AAW08109;

XX

DT 10-OCT-1997 (first entry)

XX

DE Human parathyroid hormone derivative, [Glu10]hPTH(1-34).

XX

KW Human; parathyroid hormone; PTH; cAMP-producing activity;
KW bone formation; osteoporosis; hypoparathyroidism; hypertension;
KW climacteric disturbance.

XX

OS Synthetic.

XX

PN EP748817-A2.

XX

PD 18-DEC-1996.

XX

PF 13-JUN-1996; 96EP-0109475.

XX

PR 15-JUN-1995; 95JP-0148652.

XX

PA (TAKE) TAKEDA CHEM IND LTD.

XX

PI Fukuda T, Habashita J, Nakagawa S, Taketomi S;

XX

DR WPI; 1997-036114/04.

XX

PT New parathyroid hormone derivs. - useful in treatment of bone
PT diseases, hypoparathyroidism and hypertension

XX

PS Claim 28; Page 26; 42pp; English.

XX

CC The sequences given in AAW08108-32 represent derivatives of human
CC parathyroid hormone (PTH). These peptides are human PTH (1-34)
CC derivative peptides. They have potent cAMP-producing activity and
CC bone formation activity. They may be used in treatment of bone
CC diseases including osteoporosis, hypoparathyroidism, hypertension
CC and climacteric disturbance. The peptides are low in toxicity and

CC are safe.

XX

SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 18; Length 34;

Best Local Similarity 100.0%; Pred. No. 3.4e-17;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34

||||||||||||||||||||

Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

Search completed: January 14, 2004, 10:34:19

Job time : 33.5171 secs

OM protein - protein search, using sw model

Run on: January 14, 2004, 10:28:59 ; Search time 11.5452 Seconds
(without alignments)
124.604 Million cell updates/sec

Title: US-09-843-221A-162
Perfect score: 34
Sequence: 1 SVSEIQLMHNRGKHLNSMERVEWLRKKLQDVHNF 34

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 25778

Minimum DB seq length: 28
Maximum DB seq length: 40

Post-processing: Listing first 1000 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	23	67.6	33	1	US-08-256-363-1	Sequence 1, Appli
2	23	67.6	34	1	US-07-765-373-1	Sequence 1, Appli
3	23	67.6	34	1	US-08-033-099-1	Sequence 1, Appli
4	23	67.6	34	1	US-08-262-495C-1	Sequence 1, Appli
5	23	67.6	34	1	US-07-915-247A-1	Sequence 1, Appli
6	23	67.6	34	1	US-08-443-863-1	Sequence 1, Appli
7	23	67.6	34	1	US-08-448-070-1	Sequence 1, Appli
8	23	67.6	34	1	US-08-488-105-7	Sequence 7, Appli
9	23	67.6	34	1	US-08-468-275-6	Sequence 6, Appli
10	23	67.6	34	1	US-08-256-363-2	Sequence 2, Appli
11	23	67.6	34	1	US-08-449-500-1	Sequence 1, Appli

12	23	67.6	34	1	US-08-449-317A-1	Sequence 1, Appli
13	23	67.6	34	2	US-08-142-551B-2	Sequence 2, Appli
14	23	67.6	34	2	US-08-477-022-1	Sequence 1, Appli
15	23	67.6	34	2	US-08-449-447-1	Sequence 1, Appli
16	23	67.6	34	2	US-08-835-231-13	Sequence 13, Appl
17	23	67.6	34	2	US-08-184-328-1	Sequence 1, Appli
18	23	67.6	34	2	US-08-411-726-2	Sequence 2, Appli
19	23	67.6	34	2	US-08-691-647C-5	Sequence 5, Appli
20	23	67.6	34	2	US-08-521-097-1	Sequence 1, Appli
21	23	67.6	34	3	US-09-044-536A-1	Sequence 1, Appli
22	23	67.6	34	3	US-09-044-536A-8	Sequence 8, Appli
23	23	67.6	34	3	US-09-044-536A-9	Sequence 9, Appli
24	23	67.6	34	3	US-09-044-536A-10	Sequence 10, Appl
25	23	67.6	34	3	US-09-044-536A-11	Sequence 11, Appl
26	23	67.6	34	3	US-09-044-536A-12	Sequence 12, Appl
27	23	67.6	34	3	US-09-044-536A-13	Sequence 13, Appl
28	23	67.6	34	3	US-09-044-536A-14	Sequence 14, Appl
29	23	67.6	34	3	US-09-044-536A-15	Sequence 15, Appl
30	23	67.6	34	3	US-08-904-760B-22	Sequence 22, Appl
31	23	67.6	34	3	US-09-108-661-13	Sequence 13, Appl
32	23	67.6	34	4	US-09-007-466-6	Sequence 6, Appli
33	23	67.6	34	4	US-09-406-813-1	Sequence 1, Appli
34	23	67.6	34	4	US-08-952-980B-6	Sequence 6, Appli
35	23	67.6	34	4	US-09-228-990-1	Sequence 1, Appli
36	23	67.6	34	4	US-09-447-800-1	Sequence 1, Appli
37	23	67.6	34	4	US-09-447-800-2	Sequence 2, Appli
38	23	67.6	34	4	US-09-447-800-5	Sequence 5, Appli
39	23	67.6	34	4	US-09-447-800-8	Sequence 8, Appli
40	23	67.6	34	4	US-09-536-785A-22	Sequence 22, Appl
41	23	67.6	34	4	US-09-442-989-26	Sequence 26, Appl
42	23	67.6	34	5	PCT-US95-15800-22	Sequence 22, Appl
43	23	67.6	35	1	US-08-256-363-3	Sequence 3, Appli
44	23	67.6	36	1	US-08-112-024-2	Sequence 2, Appli
45	23	67.6	36	1	US-08-256-363-4	Sequence 4, Appli
46	23	67.6	37	1	US-08-440-117-1	Sequence 1, Appli
47	23	67.6	37	3	US-09-068-738A-16	Sequence 16, Appl
48	23	67.6	38	1	US-08-112-024-1	Sequence 1, Appli
49	23	67.6	38	1	US-08-232-849-1	Sequence 1, Appli
50	23	67.6	38	2	US-08-625-586-1	Sequence 1, Appli
51	23	67.6	38	3	US-09-128-401-1	Sequence 1, Appli
52	23	67.6	38	5	PCT-US95-15800-29	Sequence 29, Appl
53	22	64.7	33	4	US-09-447-800-3	Sequence 3, Appli
54	22	64.7	33	4	US-09-447-800-6	Sequence 6, Appli
55	22	64.7	33	4	US-09-447-800-9	Sequence 9, Appli
56	22	64.7	34	3	US-08-903-497A-1	Sequence 1, Appli
57	22	64.7	34	4	US-09-635-076-1	Sequence 1, Appli
58	21	61.8	34	3	US-09-044-536A-26	Sequence 26, Appl
59	21	61.8	34	4	US-09-449-632-24	Sequence 24, Appl
60	20	58.8	31	1	US-08-262-495C-3	Sequence 3, Appli
61	20	58.8	31	2	US-08-691-647C-1	Sequence 1, Appli
62	20	58.8	31	2	US-08-691-647C-6	Sequence 6, Appli
63	20	58.8	31	3	US-08-904-760B-1	Sequence 1, Appli
64	20	58.8	31	3	US-08-904-760B-6	Sequence 6, Appli
65	20	58.8	31	3	US-08-904-760B-14	Sequence 14, Appl
66	20	58.8	31	3	US-08-904-760B-32	Sequence 32, Appl
67	20	58.8	31	4	US-09-406-813-2	Sequence 2, Appli
68	20	58.8	31	4	US-09-536-785A-1	Sequence 1, Appli

69	20	58.8	31	4	US-09-536-785A-6	Sequence 6, Appli
70	20	58.8	31	4	US-09-536-785A-14	Sequence 14, Appl
71	20	58.8	31	4	US-09-536-785A-32	Sequence 32, Appl
72	20	58.8	34	3	US-09-044-536A-25	Sequence 25, Appl
73	19	55.9	30	1	US-08-262-495C-5	Sequence 5, Appli
74	19	55.9	34	3	US-08-903-497A-3	Sequence 3, Appli
75	19	55.9	34	4	US-09-635-076-3	Sequence 3, Appli
76	18	52.9	34	1	US-07-915-247A-2	Sequence 2, Appli
77	18	52.9	34	1	US-08-443-863-2	Sequence 2, Appli
78	18	52.9	34	1	US-08-448-070-2	Sequence 2, Appli
79	18	52.9	34	1	US-08-488-105-2	Sequence 2, Appli
80	18	52.9	34	1	US-08-488-105-8	Sequence 8, Appli
81	18	52.9	34	1	US-08-449-500-2	Sequence 2, Appli
82	18	52.9	34	1	US-08-449-317A-2	Sequence 2, Appli
83	18	52.9	34	2	US-08-477-022-2	Sequence 2, Appli
84	18	52.9	34	2	US-08-449-447-2	Sequence 2, Appli
85	18	52.9	34	2	US-08-184-328-2	Sequence 2, Appli
86	18	52.9	34	2	US-08-521-097-2	Sequence 2, Appli
87	18	52.9	34	3	US-09-044-536A-18	Sequence 18, Appl
88	18	52.9	34	3	US-09-044-536A-19	Sequence 19, Appl
89	17	50.0	28	4	US-09-448-867-8	Sequence 8, Appli
90	17	50.0	28	4	US-09-448-867-10	Sequence 10, Appl
91	17	50.0	28	4	US-09-448-867-12	Sequence 12, Appl
92	17	50.0	34	1	US-08-488-105-1	Sequence 1, Appli
93	17	50.0	34	1	US-08-488-105-13	Sequence 13, Appl
94	17	50.0	34	1	US-08-488-105-14	Sequence 14, Appl
95	17	50.0	34	3	US-09-044-536A-16	Sequence 16, Appl
96	17	50.0	34	3	US-09-044-536A-17	Sequence 17, Appl
97	16	47.1	34	1	US-07-915-247A-3	Sequence 3, Appli
98	16	47.1	34	1	US-08-443-863-3	Sequence 3, Appli
99	16	47.1	34	1	US-08-448-070-3	Sequence 3, Appli
100	16	47.1	34	1	US-08-449-500-3	Sequence 3, Appli
101	16	47.1	34	1	US-08-449-317A-3	Sequence 3, Appli
102	16	47.1	34	2	US-08-477-022-3	Sequence 3, Appli
103	16	47.1	34	2	US-08-449-447-3	Sequence 3, Appli
104	16	47.1	34	2	US-08-184-328-3	Sequence 3, Appli
105	16	47.1	34	2	US-08-521-097-3	Sequence 3, Appli
106	15	44.1	28	4	US-09-406-813-3	Sequence 3, Appli
107	15	44.1	29	4	US-09-406-813-4	Sequence 4, Appli
108	15	44.1	30	1	US-08-262-495C-6	Sequence 6, Appli
109	15	44.1	30	3	US-08-904-760B-7	Sequence 7, Appli
110	15	44.1	30	4	US-09-536-785A-7	Sequence 7, Appli
111	15	44.1	31	1	US-08-262-495C-4	Sequence 4, Appli
112	15	44.1	31	2	US-08-691-647C-2	Sequence 2, Appli
113	15	44.1	31	2	US-08-691-647C-3	Sequence 3, Appli
114	15	44.1	31	2	US-08-691-647C-4	Sequence 4, Appli
115	15	44.1	31	3	US-08-904-760B-2	Sequence 2, Appli
116	15	44.1	31	3	US-08-904-760B-3	Sequence 3, Appli
117	15	44.1	31	3	US-08-904-760B-4	Sequence 4, Appli
118	15	44.1	31	3	US-08-904-760B-5	Sequence 5, Appli
119	15	44.1	31	3	US-08-904-760B-8	Sequence 8, Appli
120	15	44.1	31	3	US-08-904-760B-11	Sequence 11, Appl
121	15	44.1	31	3	US-08-904-760B-12	Sequence 12, Appl
122	15	44.1	31	3	US-08-904-760B-15	Sequence 15, Appl
123	15	44.1	31	3	US-08-904-760B-16	Sequence 16, Appl
124	15	44.1	31	3	US-08-904-760B-17	Sequence 17, Appl
125	15	44.1	31	4	US-09-536-785A-2	Sequence 2, Appli

126	15	44.1	31	4	US-09-536-785A-3	Sequence 3, Appli
127	15	44.1	31	4	US-09-536-785A-4	Sequence 4, Appli
128	15	44.1	31	4	US-09-536-785A-5	Sequence 5, Appli
129	15	44.1	31	4	US-09-536-785A-8	Sequence 8, Appli
130	15	44.1	31	4	US-09-536-785A-11	Sequence 11, Appl
131	15	44.1	31	4	US-09-536-785A-12	Sequence 12, Appl
132	15	44.1	31	4	US-09-536-785A-15	Sequence 15, Appl
133	15	44.1	31	4	US-09-536-785A-16	Sequence 16, Appl
134	15	44.1	31	4	US-09-536-785A-17	Sequence 17, Appl
135	15	44.1	34	1	US-08-262-495C-2	Sequence 2, Appli
136	15	44.1	34	1	US-08-488-105-4	Sequence 4, Appli
137	15	44.1	34	1	US-08-488-105-6	Sequence 6, Appli
138	15	44.1	34	1	US-08-488-105-10	Sequence 10, Appl
139	15	44.1	34	1	US-08-488-105-11	Sequence 11, Appl
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142	15	44.1	34	1	US-08-449-500-79	Sequence 79, Appl
143	15	44.1	34	1	US-08-449-317A-79	Sequence 79, Appl
144	15	44.1	34	2	US-08-142-551B-3	Sequence 3, Appli
145	15	44.1	34	2	US-08-477-022-79	Sequence 79, Appl
146	15	44.1	34	2	US-08-449-447-79	Sequence 79, Appl
147	15	44.1	34	2	US-08-184-328-79	Sequence 79, Appl
148	15	44.1	34	2	US-08-521-097-79	Sequence 79, Appl
149	15	44.1	34	3	US-09-044-536A-27	Sequence 27, Appl
150	15	44.1	34	3	US-08-904-760B-9	Sequence 9, Appli
151	15	44.1	34	3	US-08-904-760B-10	Sequence 10, Appl
152	15	44.1	34	3	US-08-903-497A-4	Sequence 4, Appli
153	15	44.1	34	4	US-09-635-076-4	Sequence 4, Appli
154	15	44.1	34	4	US-09-536-785A-9	Sequence 9, Appli
155	15	44.1	34	4	US-09-536-785A-10	Sequence 10, Appl
156	15	44.1	35	2	US-08-142-551B-4	Sequence 4, Appli
157	15	44.1	35	2	US-08-142-551B-5	Sequence 5, Appli
158	15	44.1	35	2	US-08-142-551B-7	Sequence 7, Appli
159	15	44.1	35	2	US-08-142-551B-11	Sequence 11, Appl
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171	15	44.1	35	2	US-08-142-551B-23	Sequence 23, Appl
172	15	44.1	35	2	US-08-142-551B-24	Sequence 24, Appl
173	15	44.1	35	2	US-08-142-551B-25	Sequence 25, Appl
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175	15	44.1	35	2	US-08-142-551B-27	Sequence 27, Appl
176	15	44.1	35	2	US-08-142-551B-28	Sequence 28, Appl
177	15	44.1	35	2	US-08-142-551B-29	Sequence 29, Appl
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180	15	44.1	35	2	US-08-142-551B-32	Sequence 32, Appl
181	15	44.1	35	2	US-08-142-551B-33	Sequence 33, Appl
182	15	44.1	35	2	US-08-142-551B-34	Sequence 34, Appl

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188	15	44.1	35	2	US-08-142-551B-40	Sequence 40, Appl
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203	15	44.1	35	2	US-08-142-551B-55	Sequence 55, Appl
204	15	44.1	35	2	US-08-142-551B-56	Sequence 56, Appl
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214	15	44.1	35	2	US-08-142-551B-66	Sequence 66, Appl
215	15	44.1	35	2	US-08-142-551B-67	Sequence 67, Appl
216	15	44.1	35	2	US-08-142-551B-68	Sequence 68, Appl
217	15	44.1	35	2	US-08-142-551B-70	Sequence 70, Appl
218	15	44.1	35	2	US-08-142-551B-73	Sequence 73, Appl
219	15	44.1	35	2	US-08-142-551B-80	Sequence 80, Appl
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222	14	41.2	31	3	US-08-904-760B-21	Sequence 21, Appl
223	14	41.2	31	4	US-09-536-785A-21	Sequence 21, Appl
224	14	41.2	34	3	US-09-044-536A-29	Sequence 29, Appl
225	14	41.2	35	2	US-08-142-551B-69	Sequence 69, Appl
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228	14	41.2	35	2	US-08-142-551B-116	Sequence 116, App
229	14	41.2	35	2	US-08-142-551B-117	Sequence 117, App
230	14	41.2	35	2	US-08-142-551B-118	Sequence 118, App
231	13	38.2	34	1	US-07-773-098-5	Sequence 5, Appli
232	13	38.2	34	1	US-07-773-098-6	Sequence 6, Appli
233	13	38.2	34	3	US-09-044-536A-28	Sequence 28, Appl
234	13	38.2	35	2	US-08-142-551B-72	Sequence 72, Appl
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236	13	38.2	35	2	US-08-142-551B-75	Sequence 75, Appl
237	13	38.2	35	2	US-08-142-551B-111	Sequence 111, App
238	13	38.2	35	2	US-08-142-551B-112	Sequence 112, App
239	13	38.2	35	2	US-08-142-551B-113	Sequence 113, App

240	13	38.2	35	2	US-08-142-551B-114	Sequence 114, App
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242	12	35.3	34	1	US-08-488-105-9	Sequence 9, Appli
243	12	35.3	34	1	US-08-488-105-15	Sequence 15, Appl
244	12	35.3	34	3	US-08-903-497A-5	Sequence 5, Appli
245	12	35.3	34	4	US-09-635-076-5	Sequence 5, Appli
246	12	35.3	35	2	US-08-142-551B-76	Sequence 76, Appl
247	12	35.3	35	2	US-08-142-551B-77	Sequence 77, Appl
248	12	35.3	35	2	US-08-142-551B-78	Sequence 78, Appl
249	12	35.3	35	2	US-08-142-551B-107	Sequence 107, App
250	12	35.3	35	2	US-08-142-551B-108	Sequence 108, App
251	12	35.3	35	2	US-08-142-551B-109	Sequence 109, App
252	12	35.3	35	2	US-08-142-551B-110	Sequence 110, App
253	11	32.4	34	1	US-08-488-105-5	Sequence 5, Appli
254	11	32.4	34	1	US-08-488-105-12	Sequence 12, Appl
255	11	32.4	34	1	US-08-488-105-17	Sequence 17, Appl
256	11	32.4	34	1	US-08-449-500-61	Sequence 61, Appl
257	11	32.4	34	1	US-08-449-317A-61	Sequence 61, Appl
258	11	32.4	34	2	US-08-477-022-61	Sequence 61, Appl
259	11	32.4	34	2	US-08-449-447-61	Sequence 61, Appl
260	11	32.4	34	2	US-08-184-328-61	Sequence 61, Appl
261	11	32.4	34	2	US-08-521-097-61	Sequence 61, Appl
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263	11	32.4	35	2	US-08-142-551B-79	Sequence 79, Appl
264	11	32.4	35	2	US-08-142-551B-81	Sequence 81, Appl
265	11	32.4	35	2	US-08-142-551B-104	Sequence 104, App
266	11	32.4	35	2	US-08-142-551B-105	Sequence 105, App
267	11	32.4	35	2	US-08-142-551B-106	Sequence 106, App
268	11	32.4	35	2	US-08-142-551B-121	Sequence 121, App
269	11	32.4	35	2	US-08-142-551B-122	Sequence 122, App
270	11	32.4	35	2	US-08-142-551B-123	Sequence 123, App
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272	10	29.4	28	4	US-09-448-867-6	Sequence 6, Appli
273	10	29.4	30	3	US-08-904-760B-33	Sequence 33, Appl
274	10	29.4	30	3	US-08-904-760B-34	Sequence 34, Appl
275	10	29.4	30	3	US-08-904-760B-35	Sequence 35, Appl
276	10	29.4	30	4	US-09-536-785A-33	Sequence 33, Appl
277	10	29.4	30	4	US-09-536-785A-34	Sequence 34, Appl
278	10	29.4	30	4	US-09-536-785A-35	Sequence 35, Appl
279	10	29.4	31	3	US-08-904-760B-18	Sequence 18, Appl
280	10	29.4	31	3	US-08-904-760B-19	Sequence 19, Appl
281	10	29.4	31	3	US-08-904-760B-20	Sequence 20, Appl
282	10	29.4	31	4	US-09-406-813-5	Sequence 5, Appli
283	10	29.4	31	4	US-09-536-785A-18	Sequence 18, Appl
284	10	29.4	31	4	US-09-536-785A-19	Sequence 19, Appl
285	10	29.4	31	4	US-09-536-785A-20	Sequence 20, Appl
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287	10	29.4	34	3	US-09-044-536A-21	Sequence 21, Appl
288	10	29.4	34	3	US-09-044-536A-22	Sequence 22, Appl
289	10	29.4	34	3	US-09-044-536A-24	Sequence 24, Appl
290	10	29.4	34	3	US-08-903-497A-6	Sequence 6, Appli
291	10	29.4	34	3	US-08-903-497A-7	Sequence 7, Appli
292	10	29.4	34	4	US-08-952-980B-9	Sequence 9, Appli
293	10	29.4	34	4	US-09-635-076-6	Sequence 6, Appli
294	10	29.4	34	4	US-09-635-076-7	Sequence 7, Appli
295	10	29.4	35	2	US-08-142-551B-82	Sequence 82, Appl
296	10	29.4	35	2	US-08-142-551B-83	Sequence 83, Appl

297	10	29.4	35	2	US-08-142-551B-84	Sequence 84, Appl
298	10	29.4	35	2	US-08-142-551B-101	Sequence 101, App
299	10	29.4	35	2	US-08-142-551B-102	Sequence 102, App
300	10	29.4	35	2	US-08-142-551B-103	Sequence 103, App
301	10	29.4	35	2	US-08-142-551B-120	Sequence 120, App
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303	9	26.5	28	4	US-09-448-867-2	Sequence 2, Appli
304	9	26.5	28	4	US-09-448-867-4	Sequence 4, Appli
305	9	26.5	34	3	US-09-044-536A-2	Sequence 2, Appli
306	9	26.5	34	3	US-09-044-536A-23	Sequence 23, Appl
307	9	26.5	35	2	US-08-142-551B-85	Sequence 85, Appl
308	9	26.5	35	2	US-08-142-551B-86	Sequence 86, Appl
309	9	26.5	35	2	US-08-142-551B-87	Sequence 87, Appl
310	9	26.5	35	2	US-08-142-551B-98	Sequence 98, Appl
311	9	26.5	35	2	US-08-142-551B-99	Sequence 99, Appl
312	9	26.5	35	2	US-08-142-551B-100	Sequence 100, App
313	9	26.5	35	3	US-09-044-536A-30	Sequence 30, Appl
314	9	26.5	36	3	US-09-044-536A-31	Sequence 31, Appl
315	9	26.5	37	3	US-09-044-536A-32	Sequence 32, Appl
316	9	26.5	38	3	US-09-044-536A-33	Sequence 33, Appl
317	9	26.5	39	3	US-09-044-536A-34	Sequence 34, Appl
318	9	26.5	40	3	US-09-044-536A-35	Sequence 35, Appl
319	8	23.5	31	3	US-08-904-760B-13	Sequence 13, Appl
320	8	23.5	31	4	US-09-228-990-50	Sequence 50, Appl
321	8	23.5	31	4	US-09-228-990-51	Sequence 51, Appl
322	8	23.5	31	4	US-09-228-990-66	Sequence 66, Appl
323	8	23.5	31	4	US-09-228-990-67	Sequence 67, Appl
324	8	23.5	31	4	US-09-228-990-76	Sequence 76, Appl
325	8	23.5	31	4	US-09-536-785A-13	Sequence 13, Appl
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327	8	23.5	34	1	US-07-773-098-4	Sequence 4, Appli
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329	8	23.5	34	1	US-08-526-987-2	Sequence 2, Appli
330	8	23.5	35	2	US-08-142-551B-88	Sequence 88, Appl
331	8	23.5	35	2	US-08-142-551B-89	Sequence 89, Appl
332	8	23.5	35	2	US-08-142-551B-95	Sequence 95, Appl
333	8	23.5	35	2	US-08-142-551B-96	Sequence 96, Appl
334	8	23.5	35	2	US-08-142-551B-97	Sequence 97, Appl
335	7	20.6	28	4	US-09-228-990-65	Sequence 65, Appl
336	7	20.6	28	4	US-09-228-990-78	Sequence 78, Appl
337	7	20.6	28	4	US-09-228-990-79	Sequence 79, Appl
338	7	20.6	28	4	US-09-442-989-22	Sequence 22, Appl
339	7	20.6	28	4	US-09-442-989-24	Sequence 24, Appl
340	7	20.6	28	4	US-09-442-989-25	Sequence 25, Appl
341	7	20.6	29	4	US-09-406-813-8	Sequence 8, Appli
342	7	20.6	31	4	US-09-406-813-9	Sequence 9, Appli
343	7	20.6	32	1	US-08-305-799A-1	Sequence 1, Appli
344	7	20.6	32	1	US-08-305-799A-2	Sequence 2, Appli
345	7	20.6	34	1	US-08-033-099-2	Sequence 2, Appli
346	7	20.6	34	1	US-08-468-275-7	Sequence 7, Appli
347	7	20.6	34	1	US-08-468-275-8	Sequence 8, Appli
348	7	20.6	34	4	US-09-007-466-7	Sequence 7, Appli
349	7	20.6	34	4	US-09-007-466-8	Sequence 8, Appli
350	7	20.6	34	4	US-09-228-990-46	Sequence 46, Appl
351	7	20.6	34	4	US-09-228-990-75	Sequence 75, Appl
352	7	20.6	34	4	US-09-442-989-18	Sequence 18, Appl
353	7	20.6	34	4	US-09-442-989-19	Sequence 19, Appl

354	7	20.6	34	4	US-09-442-989-46	Sequence 46, Appl
355	7	20.6	35	2	US-08-142-551B-10	Sequence 10, Appl
356	7	20.6	35	2	US-08-142-551B-91	Sequence 91, Appl
357	7	20.6	35	2	US-08-142-551B-92	Sequence 92, Appl
358	7	20.6	35	2	US-08-142-551B-93	Sequence 93, Appl
359	7	20.6	35	2	US-08-142-551B-124	Sequence 124, App
360	7	20.6	35	4	US-08-952-980B-7	Sequence 7, Appli
361	7	20.6	35	4	US-08-952-980B-8	Sequence 8, Appli
362	6	17.6	28	4	US-09-228-990-54	Sequence 54, Appl
363	6	17.6	28	4	US-09-228-990-62	Sequence 62, Appl
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366	6	17.6	30	4	US-09-228-990-52	Sequence 52, Appl
367	6	17.6	30	4	US-09-228-990-64	Sequence 64, Appl
368	6	17.6	30	4	US-09-536-785A-23	Sequence 23, Appl
369	6	17.6	31	3	US-08-904-760B-23	Sequence 23, Appl
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374	6	17.6	31	4	US-09-228-990-6	Sequence 6, Appli
375	6	17.6	31	4	US-09-228-990-7	Sequence 7, Appli
376	6	17.6	31	4	US-09-228-990-8	Sequence 8, Appli
377	6	17.6	31	4	US-09-228-990-9	Sequence 9, Appli
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383	6	17.6	31	4	US-09-228-990-15	Sequence 15, Appl
384	6	17.6	31	4	US-09-228-990-16	Sequence 16, Appl
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386	6	17.6	31	4	US-09-228-990-18	Sequence 18, Appl
387	6	17.6	31	4	US-09-228-990-19	Sequence 19, Appl
388	6	17.6	31	4	US-09-228-990-20	Sequence 20, Appl
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390	6	17.6	31	4	US-09-228-990-22	Sequence 22, Appl
391	6	17.6	31	4	US-09-228-990-23	Sequence 23, Appl
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393	6	17.6	31	4	US-09-228-990-25	Sequence 25, Appl
394	6	17.6	31	4	US-09-228-990-26	Sequence 26, Appl
395	6	17.6	31	4	US-09-228-990-27	Sequence 27, Appl
396	6	17.6	31	4	US-09-228-990-28	Sequence 28, Appl
397	6	17.6	31	4	US-09-228-990-29	Sequence 29, Appl
398	6	17.6	31	4	US-09-228-990-30	Sequence 30, Appl
399	6	17.6	31	4	US-09-228-990-31	Sequence 31, Appl
400	6	17.6	31	4	US-09-228-990-32	Sequence 32, Appl
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418	6	17.6	31	4	US-09-228-990-69	Sequence 69, Appl
419	6	17.6	31	4	US-09-228-990-70	Sequence 70, Appl
420	6	17.6	31	4	US-09-228-990-73	Sequence 73, Appl
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435	6	17.6	31	4	US-09-442-989-4	Sequence 4, Appli
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439	6	17.6	31	4	US-09-442-989-8	Sequence 8, Appli
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518	4	11.8	28	2	US-08-620-151-126	Sequence 126, App
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524	4	11.8	28	4	US-09-323-867A-153	Sequence 153, App

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526	4	11.8	29	4	US-09-227-357-480	Sequence 480, App
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530	4	11.8	30	1	US-08-305-799A-4	Sequence 4, Appli
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534	4	11.8	31	1	US-08-248-021A-5	Sequence 5, Appli
535	4	11.8	31	1	US-08-323-531-44	Sequence 44, Appl
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540	4	11.8	31	1	US-08-198-094-62	Sequence 62, Appl
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543	4	11.8	31	2	US-08-663-566A-32	Sequence 32, Appl
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549	4	11.8	31	3	US-08-107-794A-62	Sequence 62, Appl
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554	4	11.8	31	5	PCT-US93-07424-62	Sequence 62, Appl
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557	4	11.8	31	5	PCT-US95-02087-62	Sequence 62, Appl
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561	4	11.8	32	1	US-08-190-802A-114	Sequence 114, App
562	4	11.8	32	1	US-08-190-802A-183	Sequence 183, App
563	4	11.8	32	1	US-08-190-802A-216	Sequence 216, App
564	4	11.8	32	3	US-08-477-346-110	Sequence 110, App
565	4	11.8	32	3	US-08-477-346-114	Sequence 114, App
566	4	11.8	32	3	US-08-477-346-183	Sequence 183, App
567	4	11.8	32	3	US-08-477-346-216	Sequence 216, App
568	4	11.8	32	4	US-08-473-089-110	Sequence 110, App
569	4	11.8	32	4	US-08-473-089-114	Sequence 114, App
570	4	11.8	32	4	US-08-473-089-183	Sequence 183, App
571	4	11.8	32	4	US-08-473-089-216	Sequence 216, App
572	4	11.8	32	4	US-09-149-476-442	Sequence 442, App
573	4	11.8	32	4	US-08-487-072A-110	Sequence 110, App
574	4	11.8	32	4	US-08-487-072A-114	Sequence 114, App
575	4	11.8	32	4	US-08-487-072A-183	Sequence 183, App
576	4	11.8	32	4	US-08-487-072A-216	Sequence 216, App
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588	4	11.8	34	4	US-09-433-043B-7	Sequence 7, Appli
589	4	11.8	35	4	US-09-227-357-486	Sequence 486, App
590	4	11.8	35	4	US-09-690-454-138	Sequence 138, App
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592	4	11.8	37	1	US-08-231-730A-45	Sequence 45, Appl
593	4	11.8	37	1	US-08-237-418-16	Sequence 16, Appl
594	4	11.8	37	2	US-08-283-917-12	Sequence 12, Appl
595	4	11.8	37	2	US-08-961-716-12	Sequence 12, Appl
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599	4	11.8	37	3	US-09-340-154-50	Sequence 50, Appl
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603	4	11.8	37	4	US-09-758-318-16	Sequence 16, Appl
604	4	11.8	37	5	PCT-US95-04718-45	Sequence 45, Appl
605	4	11.8	37	5	PCT-US95-09338-50	Sequence 50, Appl
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609	4	11.8	38	2	US-08-378-548-12	Sequence 12, Appl
610	4	11.8	38	3	US-09-273-685-55	Sequence 55, Appl
611	4	11.8	38	4	US-09-463-238-8	Sequence 8, Appli
612	4	11.8	38	5	PCT-US95-11934-55	Sequence 55, Appl
613	4	11.8	39	4	US-09-227-357-384	Sequence 384, App
614	4	11.8	39	4	US-08-857-046A-25	Sequence 25, Appl
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622	3	8.8	28	1	US-07-690-300B-26	Sequence 26, Appl
623	3	8.8	28	1	US-07-690-300B-27	Sequence 27, Appl
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632	3	8.8	28	1	US-07-690-300B-36	Sequence 36, Appl
633	3	8.8	28	1	US-07-690-300B-37	Sequence 37, Appl
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635	3	8.8	28	1	US-07-690-300B-39	Sequence 39, Appl
636	3	8.8	28	1	US-07-690-300B-40	Sequence 40, Appl
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644	3	8.8	28	1	US-07-690-300B-48	Sequence 48, Appl
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652	3	8.8	28	1	US-07-690-300B-56	Sequence 56, Appl
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655	3	8.8	28	1	US-07-690-300B-68	Sequence 68, Appl
656	3	8.8	28	1	US-07-690-300B-71	Sequence 71, Appl
657	3	8.8	28	1	US-07-690-300B-78	Sequence 78, Appl
658	3	8.8	28	1	US-07-690-300B-79	Sequence 79, Appl
659	3	8.8	28	1	US-07-690-300B-82	Sequence 82, Appl
660	3	8.8	28	1	US-07-690-300B-88	Sequence 88, Appl
661	3	8.8	28	1	US-07-690-300B-91	Sequence 91, Appl
662	3	8.8	28	1	US-07-690-300B-93	Sequence 93, Appl
663	3	8.8	28	1	US-07-663-413-29	Sequence 29, Appl
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665	3	8.8	28	1	US-07-676-987A-2	Sequence 2, Appli
666	3	8.8	28	1	US-07-833-468-1	Sequence 1, Appli
667	3	8.8	28	1	US-08-052-681-10	Sequence 10, Appl
668	3	8.8	28	1	US-07-789-344A-11	Sequence 11, Appl
669	3	8.8	28	1	US-07-868-906-1	Sequence 1, Appli
670	3	8.8	28	1	US-08-201-092-1	Sequence 1, Appli
671	3	8.8	28	1	US-08-201-092-2	Sequence 2, Appli
672	3	8.8	28	1	US-08-055-530-29	Sequence 29, Appl
673	3	8.8	28	1	US-08-122-578-1	Sequence 1, Appli
674	3	8.8	28	1	US-08-255-558B-6	Sequence 6, Appli
675	3	8.8	28	1	US-07-924-054-11	Sequence 11, Appl
676	3	8.8	28	1	US-08-243-082-1	Sequence 1, Appli
677	3	8.8	28	1	US-08-246-572-4	Sequence 4, Appli
678	3	8.8	28	1	US-08-246-572-5	Sequence 5, Appli
679	3	8.8	28	1	US-08-190-802A-84	Sequence 84, Appl
680	3	8.8	28	1	US-08-361-443-1	Sequence 1, Appli
681	3	8.8	28	1	US-08-311-611A-12	Sequence 12, Appl
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683	3	8.8	28	1	US-08-311-611A-193	Sequence 193, App
684	3	8.8	28	1	US-08-311-611A-194	Sequence 194, App
685	3	8.8	28	1	US-08-311-611A-195	Sequence 195, App
686	3	8.8	28	1	US-08-311-611A-196	Sequence 196, App
687	3	8.8	28	1	US-07-949-797B-1	Sequence 1, Appli
688	3	8.8	28	1	US-08-194-591-1	Sequence 1, Appli
689	3	8.8	28	1	US-08-194-591-2	Sequence 2, Appli
690	3	8.8	28	1	US-08-257-446-6	Sequence 6, Appli
691	3	8.8	28	1	US-08-372-783-12	Sequence 12, Appl
692	3	8.8	28	1	US-08-372-783-56	Sequence 56, Appl
693	3	8.8	28	1	US-08-372-783-193	Sequence 193, App
694	3	8.8	28	1	US-08-372-783-194	Sequence 194, App
695	3	8.8	28	1	US-08-372-783-195	Sequence 195, App

696	3	8.8	28	1	US-08-372-783-196	Sequence 196, App
697	3	8.8	28	1	US-07-977-630-42	Sequence 42, Appl
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704	3	8.8	28	1	US-08-372-105-12	Sequence 12, Appl
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707	3	8.8	28	1	US-08-372-105-194	Sequence 194, App
708	3	8.8	28	1	US-08-372-105-195	Sequence 195, App
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713	3	8.8	28	1	US-08-306-473A-194	Sequence 194, App
714	3	8.8	28	1	US-08-306-473A-195	Sequence 195, App
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778	3	8.8	28	1	US-08-308-729-73	Sequence 73, Appl
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816	3	8.8	28	2	US-08-485-445A-196	Sequence 196, App
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838	3	8.8	28	2	US-08-413-708B-8	Sequence 8, Appli
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875	3	8.8	28	3	US-08-952-568-14	Sequence 14, Appl
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934	3	8.8	28	3	US-08-485-264A-136	Sequence 136, App
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939	3	8.8	28	3	US-09-041-886-39	Sequence 39, Appl
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944	3	8.8	28	3	US-09-041-886-53	Sequence 53, Appl
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946	3	8.8	28	3	US-09-041-886-56	Sequence 56, Appl
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948	3	8.8	28	3	US-07-966-049A-9	Sequence 9, Appli
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957	3	8.8	28	3	US-09-082-279B-1280	Sequence 1280, Ap
958	3	8.8	28	3	US-09-082-279B-1314	Sequence 1314, Ap
959	3	8.8	28	3	US-09-082-279B-1315	Sequence 1315, Ap
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961	3	8.8	28	3	US-09-127-926-19	Sequence 19, Appl
962	3	8.8	28	3	US-08-894-997-43	Sequence 43, Appl
963	3	8.8	28	3	US-09-217-352-30	Sequence 30, Appl
964	3	8.8	28	3	US-09-217-352-139	Sequence 139, App
965	3	8.8	28	3	US-09-217-352-140	Sequence 140, App
966	3	8.8	28	3	US-09-217-352-142	Sequence 142, App
967	3	8.8	28	3	US-09-217-352-143	Sequence 143, App
968	3	8.8	28	4	US-09-406-781-10	Sequence 10, Appl
969	3	8.8	28	4	US-09-406-781-11	Sequence 11, Appl
970	3	8.8	28	4	US-09-260-846-16	Sequence 16, Appl
971	3	8.8	28	4	US-08-474-349A-84	Sequence 84, Appl
972	3	8.8	28	4	US-08-474-349A-136	Sequence 136, App
973	3	8.8	28	4	US-09-099-041A-23	Sequence 23, Appl
974	3	8.8	28	4	US-09-187-789-23	Sequence 23, Appl
975	3	8.8	28	4	US-08-473-089-84	Sequence 84, Appl
976	3	8.8	28	4	US-09-227-357-481	Sequence 481, App
977	3	8.8	28	4	US-09-227-357-531	Sequence 531, App
978	3	8.8	28	4	US-09-315-304B-54	Sequence 54, Appl
979	3	8.8	28	4	US-09-315-304B-62	Sequence 62, Appl
980	3	8.8	28	4	US-09-315-304B-982	Sequence 982, App

981	3	8.8	28	4	US-09-315-304B-1279	Sequence 1279, Ap
982	3	8.8	28	4	US-09-315-304B-1280	Sequence 1280, Ap
983	3	8.8	28	4	US-09-315-304B-1314	Sequence 1314, Ap
984	3	8.8	28	4	US-09-315-304B-1315	Sequence 1315, Ap
985	3	8.8	28	4	US-09-432-879-8	Sequence 8, Appli
986	3	8.8	28	4	US-08-979-608A-26	Sequence 26, Appl
987	3	8.8	28	4	US-09-245-281-23	Sequence 23, Appl
988	3	8.8	28	4	US-08-842-322-31	Sequence 31, Appl
989	3	8.8	28	4	US-09-280-909A-19	Sequence 19, Appl
990	3	8.8	28	4	US-09-333-842-1	Sequence 1, Appli
991	3	8.8	28	4	US-09-685-027-22	Sequence 22, Appl
992	3	8.8	28	4	US-08-487-072A-84	Sequence 84, Appl
993	3	8.8	28	4	US-09-446-352B-1	Sequence 1, Appli
994	3	8.8	28	4	US-09-139-600-18	Sequence 18, Appl
995	3	8.8	28	4	US-09-288-143-131	Sequence 131, App
996	3	8.8	28	4	US-08-255-208A-20	Sequence 20, Appl
997	3	8.8	28	4	US-08-469-260A-573	Sequence 573, App
998	3	8.8	28	4	US-09-101-751A-28	Sequence 28, Appl
999	3	8.8	28	4	US-09-207-359B-23	Sequence 23, Appl
1000	3	8.8	28	4	US-09-316-919-53	Sequence 53, Appl

ALIGNMENTS

RESULT 1

US-08-256-363-1

; Sequence 1, Application US/08256363

; Patent No. 5783558

; GENERAL INFORMATION:

; APPLICANT: DUVOS, CHRISTIAN

; APPLICANT: MAYER, HUBERT

; APPLICANT: MUELLER-BECKMANN, BERND

; APPLICANT: STREIN, KLAUS

; APPLICANT: WINGENDER, EDGAR

; TITLE OF INVENTION: PARATHYROID HORMONE FRAGMENTS, THEIR

; TITLE OF INVENTION: PREPARATION AND MEDICAMENTS CONTAINING THE SAME

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NIKAIDO, MARMELESTEIN, MURRAY, AND ORAM

; STREET: 655 15th ST. N.W. SUITE 330- G ST. LOBBY

; CITY: WASHINGTON

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 2005 5701

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/256,363

; FILING DATE:

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: DE P 42 03 040.4

; FILING DATE: 04-FEB-1992

; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/EP93/00259
 ; FILING DATE: 04-FEB-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: KLESNER, SHARON N.
 ; REGISTRATION NUMBER: 36,335
 ; REFERENCE/DOCKET NUMBER: P1614-4025
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 638-5000
 ; TELEFAX: (202) 638-4810
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 33 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US-08-256-363-1

Query Match 67.6%; Score 23; DB 1; Length 33;
 Best Local Similarity 100.0%; Pred. No. 1.4e-15;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
 ||||||||||||||||||
 Db 10 GKHLNSMERVEWLRKKLQDVHNF 32

RESULT 2

US-07-765-373-1

; Sequence 1, Application US/07765373
 ; Patent No. 5393869
 ; GENERAL INFORMATION:

; APPLICANT: NAKAGAWA, Shizue
 ; APPLICANT: FUKUDA, Tsunehiko
 ; APPLICANT: KAWASE, Masahiro
 ; APPLICANT: YAMAZAKI, Iwao
 ; TITLE OF INVENTION: PARATHYROID HORMONE DERIVATIVES
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
 ; ADDRESSEE: CUSHMAN
 ; STREET: 130 Water Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: US
 ; ZIP: 02109

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/765,373
 ; FILING DATE: 19910925
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:

; NAME: WILLIAMS, Gregory D.
; REGISTRATION NUMBER: 30901
; REFERENCE/DOCKET NUMBER: 41289
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; TELEX: 20091 STRE UR
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: N-terminal
US-07-765-373-1

Query Match 67.6%; Score 23; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.4e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 3

US-08-033-099-1

; Sequence 1, Application US/08033099
; Patent No. 5434246
; GENERAL INFORMATION:
; APPLICANT: FUKUDA, Tsunehiko
; APPLICANT: NAKAGAWA, Shizue
; APPLICANT: TAKETOMI, Shigehisa
; TITLE OF INVENTION: PARATHYROID HORMONE DERIVATIVES
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G.CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/033,099
; FILING DATE: 19930316
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: WILLIAMS, Gregory D
; REGISTRATION NUMBER: 30901
; REFERENCE/DOCKET NUMBER: 42528
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617)523-3400
; TELEFAX: (613)523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: N-terminal
US-08-033-099-1

Query Match 67.6%; Score 23; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.4e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 4

US-08-262-495C-1

; Sequence 1, Application US/08262495C
; Patent No. 5556940
; GENERAL INFORMATION:
; APPLICANT: WILLICK, Gordon E.
; APPLICANT: WHITFIELD, James F.
; APPLICANT: SUREWICZ, Witold
; APPLICANT: SUNG, Wing L.
; APPLICANT: NEUGENBAUER, Witold
; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES
; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kirby, Eades, Gale, Baker
; STREET: 112 Kent Street, Suite 770,
; CITY: Ottawa
; COUNTRY: Canada
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/262,495C
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: EADES, No. 5556940ris M.
; REGISTRATION NUMBER: 5,263
; REFERENCE/DOCKET NUMBER: 36210
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (613)-237-6900
; TELEFAX: (613)-237-0045
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-262-495C-1

Query Match 67.6%; Score 23; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.4e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 5

US-07-915-247A-1

; Sequence 1, Application US/07915247A
; Patent No. 5589452
; GENERAL INFORMATION:
; APPLICANT: Krstenansky, John L.
; APPLICANT: Nestor Jr., John J.
; APPLICANT: Ho, Teresa H.
; APPLICANT: Vickery, Brian H.
; APPLICANT: Bach, Chinh T.
; TITLE OF INVENTION: ANALOGS OF PARATHYROID HORMONE AND
; TITLE OF INVENTION: PARATHYROID HORMONE RELATED PEPTIDE: SYNTHESIS AND USE
; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.
; STREET: 3401 Hillview Ave.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/915,247A
; FILING DATE: 19920714
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Schmonsees, William
; REGISTRATION NUMBER: 31,796
; REFERENCE/DOCKET NUMBER: 27610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-6593
; TELEFAX: 415-496-3529
; INFORMATION FOR SEQ ID NO: 1:

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; SEQUENCE CHARACTERISTICS:
;   LENGTH: 34 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
US-07-915-247A-1

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Query Match 67.6%; Score 23; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.4e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 6

US-08-443-863-1

; Sequence 1, Application US/08443863

; Patent No. 5693616

GENERAL INFORMATION:

APPLICANT: Krstenansky, John L.

APPLICANT: Nestor Jr., John J.

APPLICANT: Ho, Teresa H.

; APPLICANT: Vickery, Brian H.

APPLICANT: Bach, Chinh T.

10 TITLE OF INVENTION: ANALOGS OF PARATHYROID HORMONE AND

TITLE OF INVENTION: PARATHYROID HORMONE RELATED PEPTIDE: SYNTHESIS AND USE

TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS

NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:

ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.

STREET: 3401 Hillview Ave.

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94303

; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk

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COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.25

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; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/443,863

FILING DATE: 14-JUL-1992

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Schmonsees, William

REGISTRATION NUMBER: 31,796

REFERENCE/DOCKET NUMBER: 27610

: TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-6593

; TELEFAX: 415-496-3529

```

; INFORMATION FOR SEQ ID NO: 1:

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; SEQUENCE CHARACTERISTICS:

; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
US-08-443-863-1

Query Match 67.6%; Score 23; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.4e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
| | | | | | | | | | | | | | | | | | | | | |
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 7

US-08-448-070-1

; Sequence 1, Application US/08448070
; Patent No. 5695955
; GENERAL INFORMATION:
; APPLICANT: Krstenansky, John L.
; APPLICANT: Nestor Jr., John J.
; APPLICANT: Ho, Teresa H.
; APPLICANT: Vickery, Brian H.
; APPLICANT: Bach, Chinh T.
; TITLE OF INVENTION: ANALOGS OF PARATHYROID HORMONE AND
; TITLE OF INVENTION: PARATHYROID HORMONE RELATED PEPTIDE: SYNTHESIS AND USE
; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.
; STREET: 3401 Hillview Ave.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/448,070
; FILING DATE: 14-JUL-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Schmonsees, William
; REGISTRATION NUMBER: 31,796
; REFERENCE/DOCKET NUMBER: 27610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-6593
; TELEFAX: 415-496-3529
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal

US-08-448-070-1

Query Match 67.6%; Score 23; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.4e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34
| | | | | | | | | | | | | | | | | | | | | |
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 8

US-08-488-105-7

; Sequence 7, Application US/08488105
; Patent No. 5717062
; GENERAL INFORMATION:
; APPLICANT: Chorev, Michael
; APPLICANT: Rosenblatt, Michael
; TITLE OF INVENTION: CYCLIC ANALOGS OF PTH AND PTHrP
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,105
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Tsao, Y. Rocky
; REGISTRATION NUMBER: 34,053
; REFERENCE/DOCKET NUMBER: 00537/112001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:

US-08-468-275-6

Query Match 67.6%; Score 23; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.4e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 10

US-08-256-363-2

; Sequence 2, Application US/08256363

; Patent No. 5783558

; GENERAL INFORMATION:

APPLICANT: DUVOS, CHRISTIAN

APPLICANT: MAYER, HUBERT

APPLICANT: MUELLER-BECKMANN, BERND

APPLICANT: STREIN, KLAUS

APPLICANT: WINGENDER, EDGAR

TITLE OF INVENTION: PARATHYROID HORMONE FRAGMENTS, THEIR

TITLE OF INVENTION: PREPARATION AND MEDICAMENTS CONTAINING THE SAME

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIKAIDO, MARMELSTEIN, MURRAY, AND ORAM

STREET: 655 15th ST. N.W. SUITE 330- G ST. LOBBY

CITY: WASHINGTON

; STATE: D.C.

COUNTRY: U.S.A.

; ZIP: 2005 5701

; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.25

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; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/256,363

; FILING DATE:

CLASSIFICATION: 514

;
PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE P 42 03 040.4

FILING DATE: 04-FEB-1992

; PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/EP93/00259

FILING DATE: 04-FEB-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: KLESNER, SHARON N.

REGISTRATION NUMBER: 36,335

REFERENCE/DOCKET NUMBER: P1614-4025

; TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 638-5000

TELEFAX: (202) 638-4810

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

LENGTH: 34 amino acids

; TYPE: amino acid

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-256-363-2

Query Match 67.6%; Score 23; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.4e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||
Db 10 GKHLNSMERVEWLRKKLQDVHNF 32

RESULT 11

US-08-449-500-1

; Sequence 1, Application US/08449500
; Patent No. 5798225

; GENERAL INFORMATION:

; APPLICANT: Krstenansky, John L.
; APPLICANT: Nestor Jr., John J.
; APPLICANT: Ho, Teresa H.
; APPLICANT: Vickery, Brian H.
; APPLICANT: Bach, Chinh T.

; TITLE OF INVENTION: ANALOGS OF PARATHYROID HORMONE AND
; TITLE OF INVENTION: PARATHYROID HORMONE RELATED PEPTIDE: SYNTHESIS AND USE
; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS
; NUMBER OF SEQUENCES: 86

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.
; STREET: 3401 Hillyview Ave.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94303

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/449,500
; FILING DATE: 18-JAN-1994
; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Schmonsees, William
; REGISTRATION NUMBER: 31,796
; REFERENCE/DOCKET NUMBER: 27610-P1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-855-6593
; TELEFAX: 415-496-3529

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
US-08-449-500-1

Query Match 67.6%; Score 23; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.4e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 12

US-08-449-317A-1

; Sequence 1, Application US/08449317A
; Patent No. 5807823
; GENERAL INFORMATION:
; APPLICANT: Vickery, Brian H.
; TITLE OF INVENTION: METHOD FOR TREATMENT OF CORTICOSTEROID
; TITLE OF INVENTION: INDUCED OSTEOPENIA
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.
; STREET: 3401 Hillview Ave.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,317A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Schmonsees, William
; REGISTRATION NUMBER: 31,796
; REFERENCE/DOCKET NUMBER: 27610-P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-6593
; TELEFAX: 415-496-3529
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
US-08-449-317A-1

Query Match 67.6%; Score 23; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.4e-15;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
| | | | | | | | | | | | | | | | | |
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 13

US-08-142-551B-2

; Sequence 2, Application US/08142551B

; Patent No. 5814603

; GENERAL INFORMATION:

; APPLICANT: Oldenburg, Kevin R.

; APPLICANT: Selick, Harold E.

; TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND

; TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME

; NUMBER OF SEQUENCES: 132

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Burns, Doane, Swecker & Mathis

; STREET: 699 Prince Street

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: US

; ZIP: 22313

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/142,551B

; FILING DATE: 25-OCT-1993

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/077,296

; FILING DATE: 14-JUN-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/898,219

; FILING DATE: 12-JUN-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/965,677

; FILING DATE: 22-OCT-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Swiss, Gerald F.

; REGISTRATION NUMBER: 30,113

; REFERENCE/DOCKET NUMBER: 000324-010

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 854-7400

; TELEFAX: (415) 854-8275

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 34 amino acids

; TYPE: amino acid

; TOPOLOGY: unknown

; MOLECULE TYPE: protein

; FEATURE:

; NAME/KEY: Peptide

US-08-142-551B-2

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||
 Db 12 GKHLNSMERVEWLRKKLODVHNF 34

US-08-477-022-1

US-08-477-022-1

Query Match 67.6%; Score 23; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.4e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 15

US-08-449-447-1

; Sequence 1, Application US/08449447

; Patent No. 5840837

; GENERAL INFORMATION:

; APPLICANT: Krstenansky, John L.

; APPLICANT: Nestor Jr., John J.

; APPLICANT: Ho, Teresa H.

; APPLICANT: Vickery, Brian H.

; APPLICANT: Bach, Chinh T.

; TITLE OF INVENTION: ANALOGS OF PARATHYROID HORMONE AND

; TITLE OF INVENTION: PARATHYROID HORMONE RELATED PEPTIDE: SYNTHESIS AND USE

; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS

; NUMBER OF SEQUENCES: 86

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.

; STREET: 3401 Hillview Ave.

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94303

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/449,447

; FILING DATE: 18-JAN-1994

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Schmonsees, William

; REGISTRATION NUMBER: 31,796

; REFERENCE/DOCKET NUMBER: 27610-P1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-855-6593

; TELEFAX: 415-496-3529

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 34 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; FRAGMENT TYPE: N-terminal

US-08-449-447-1

Query Match 67.6%; Score 23; DB 2; Length 34;

Best Local Similarity 100.0%; Pred. No. 1.4e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
| | | | | | | | | | | | | | | | | | | | | |
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 16

US-08-835-231-13

; Sequence 13, Application US/08835231

; Patent No. 5861284

; GENERAL INFORMATION:

; APPLICANT: NISHIMURA, Osamu

; APPLICANT: KURIYAMA, Masato

; APPLICANT: KOYAMA, No. 5861284uyuki

; APPLICANT: FUKUDA, Tsunehiko

; TITLE OF INVENTION: METHOD FOR PRODUCING A BIOLOGICALLY

; TITLE OF INVENTION: ACTIVE RECOMBINANT CYSTEINE-FREE

; NUMBER OF SEQUENCES: 37

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP

; STREET: 130 WATER STREET

; CITY: BOSTON

; STATE: MA

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/835,231

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/350,709

; FILING DATE: 07-DEC-1994

; APPLICATION NUMBER: 07/838,857

; FILING DATE: 18-FEB-1992

; APPLICATION NUMBER: JP 024841

; FILING DATE: 19-FEB-1991

; APPLICATION NUMBER: JP 0271438

; FILING DATE: 18-OCT-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: DAVID, RESNICK S

; REGISTRATION NUMBER: 34,235

; REFERENCE/DOCKET NUMBER: 41614-FWC

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-523-3400

; TELEFAX: 617-523-6440

; TELEX: 200291 STRE

; INFORMATION FOR SEQ ID NO: 13:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 34 amino acids

; TYPE: amino acid

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:

US-08-835-231-13

Query Match 67.6%; Score 23; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.4e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
| | | | | | | | | | | | | | | | | |
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 17

US-08-184-328-1

; Sequence 1, Application US/08184328

; Patent No. 5874086

; GENERAL INFORMATION:

; APPLICANT: Krstenansky, John L.

; APPLICANT: Nestor Jr., John J.

; APPLICANT: Ho, Teresa H.

; APPLICANT: Vickery, Brian H.

; APPLICANT: Bach, Chinh T.

; TITLE OF INVENTION: ANALOGS OF PARATHYROID HORMONE AND

; TITLE OF INVENTION: PARATHYROID HORMONE RELATED PEPTIDE: SYNTHESIS AND USE

; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS

; NUMBER OF SEQUENCES: 86

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.

; STREET: 3401 Hillview Ave.

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94303

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/184,328

; FILING DATE: 18-JAN-1994

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Schmonsees, William

; REGISTRATION NUMBER: 31,796

; REFERENCE/DOCKET NUMBER: 27610-P1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-855-6593

; TELEFAX: 415-496-3529

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
US-08-184-328-1

Query Match 67.6%; Score 23; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.4e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
| | | | | | | | | | | | | | | | | |
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 18

US-08-411-726-2

; Sequence 2, Application US/08411726
; Patent No. 5880093
; GENERAL INFORMATION:
; APPLICANT: BAGNOLI, Franco
; TITLE OF INVENTION: Use of Parathormone, Its Biologically
; TITLE OF INVENTION: Active Fragments and Correlated Peptides, for The
Preparation of
; TITLE OF INVENTION: Pharmaceutical Compositions Useful for The Treatment
of Pregnanc
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenyon & Kenyon
; STREET: 1 Broadway
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
; SOFTWARE: WordPerfect 6.1 for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/411,726
; FILING DATE: 05-APR-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/02755
; FILING DATE: 08-OCT-1993
; APPLICATION NUMBER: MI-92A002331
; FILING DATE: 09-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: PALMESE, Maria Luisa
; REGISTRATION NUMBER: 34,402
; REFERENCE/DOCKET NUMBER: 2111/1300
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-425-7200
; TELEFAX: 212-425-5288

```

; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-411-726-2

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Query Match 67.6%; Score 23; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.4e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	12	GKHLNSMERVEWLRKKLQDVHNF	34
Db	12	GKHLNSMERVEWLRKKLODVHNF	34

RESULT 19

US-08-691-647C-5

; Sequence 5, Application US/08691647C

; Patent No. 5955425

; GENERAL INFORMATION:

; APPLICANT: Barbier, Jean-Rene

APPLICANT: Morley, Paul

APPLICANT: Neugebauer, Witold

APPLICANT: Ross, Virginia

; APPLICANT: Whitfield, James

; APPLICANT: Willick, Gordon E.

TITLE OF INVENTION: CYCLIC PARATHYROID HORMONE ANALOGUES

TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NIXON & VANDERHYE, P.C.

; STREET: 1100 New York Avenue, 8th Floor

; CITY: Arlington

STATE: Virginia

; COUNTRY: U.S.A.

ZIP: 22201-4714

; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

```

;      COMPUTER:  IBM PC compatible

```

OPERATING SYSTEM: PC-DOS/MS-DOS

```

: SOFTWARE: ASCII Text

```

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/691,647C

FILING DATE: August 2, 1996

CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

NAME: Crawford, Arthur R.

REGISTRATION NUMBER: 25,327

REFERENCE/DOCKET NUMBER: 1339-5

; TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 816-4005

; TELEFAX: (703) 816-4100

; TELEX: N/A

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-691-647C-5

Query Match 67.6%; Score 23; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.4e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 20

US-08-521-097-1

; Sequence 1, Application US/08521097

; Patent No. 5977070

; GENERAL INFORMATION:

; APPLICANT: Krstenansky, John L.

; APPLICANT: Nestor Jr., John J.

; APPLICANT: Ho, Teresa H.

; APPLICANT: Vickery, Brian H.

; APPLICANT: Bach, Chinh T.

; TITLE OF INVENTION: ANALOGS OF PARATHYROID HORMONE AND

; TITLE OF INVENTION: PARATHYROID HORMONE RELATED PEPTIDE: SYNTHESIS AND USE

; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS

; NUMBER OF SEQUENCES: 86

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.

; STREET: 3401 Hillview Ave.

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94303

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/521,097

; FILING DATE: 29-AUG-1995

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/184,328

; FILING DATE: 18-JAN-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Schmonsees, William

; REGISTRATION NUMBER: 31,796

; REFERENCE/DOCKET NUMBER: 27610-P1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-855-6593

; TELEFAX: 415-496-3529

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
US-08-521-097-1

Query Match 67.6%; Score 23; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.4e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 21

US-09-044-536A-1

; Sequence 1, Application US/09044536A
; Patent No. 6025467
; GENERAL INFORMATION:
; APPLICANT: FUKUDA, Tsunehiko
; APPLICANT: NAKAGAWA, Shizue
; APPLICANT: HABASHITA, Junko
; APPLICANT: TAKETOMI, Shigehisa
; TITLE OF INVENTION: PARATHYROID HORMONE DERIVATIVES AND THEIR USE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/044,536A
; FILING DATE: 19-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/662,871
; FILING DATE: 12-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: CONLIN, David G
; REGISTRATION NUMBER: 27,026
; REFERENCE/DOCKET NUMBER: 46509-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids

```

;      TYPE:   amino acid
;      STRANDEDNESS:
;      TOPOLOGY: linear
;      MOLECULE TYPE: peptide
;      FEATURE:
;      NAME/KEY: partial peptide
;      LOCATION: 1..34
US-09-044-536A-1

```

Query Match 67.6%; Score 23; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.4e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34
 | | | | | | | | | | | | | | |
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 22

US-09-044-536A-8

: Sequence 8, Application US/09044536A

Patent No. 6025467

; GENERAL INFORMATION:

APPLICANT: FUKUDA, Tsunehiko

APPLICANT: NAKAGAWA, Shizue

APPLICANT: HABASHITA, Junko

APPLICANT: TAKETOMI, Shigehisa

TITLE OF INVENTION: PARATHYROID HORMONE DERIVATIVES AND THEIR USE

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN

STREET: 130 Water Street

CITY: Boston

STATE: Massachusetts

COUNTRY: US

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

```

; COMPUTER: IBM PC compatible

```

OPERATING SYSTEM: PC-DOS/MS-DOS

```

; SOFTWARE: PatentIn Release #1.0, Version #1.30

```

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/044,536A

FILING DATE: 19-MAR-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/662,871

FILING DATE: 12-JUN-1996

ATTORNEY/AGENT INFORMATION:

; NAME: CONLIN, David G

REGISTRATION NUMBER: 27,026

REFERENCE/DOCKET NUMBER: 46509-DIV

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 523-3400

TELEFAX: (617) 523-6440

INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

LENGTH: 34 amino acids

; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: partial peptide
; LOCATION: 1..34
US-09-044-536A-8

Query Match 67.6%; Score 23; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.4e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 23

US-09-044-536A-9

; Sequence 9, Application US/09044536A
; Patent No. 6025467
; GENERAL INFORMATION:
; APPLICANT: FUKUDA, Tsunehiko
; APPLICANT: NAKAGAWA, Shizue
; APPLICANT: HABASHITA, Junko
; APPLICANT: TAKETOMI, Shigehisa
; TITLE OF INVENTION: PARATHYROID HORMONE DERIVATIVES AND THEIR USE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/044,536A
; FILING DATE: 19-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/662,871
; FILING DATE: 12-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: CONLIN, David G
; REGISTRATION NUMBER: 27,026
; REFERENCE/DOCKET NUMBER: 46509-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids

US-09-044-536A-9

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

US-09-044-536A-10

```

; Sequence 10, Application US/09044536A
; Patent No. 6025467
; GENERAL INFORMATION:
; APPLICANT: FUKUDA, Tsunehiko
; APPLICANT: NAKAGAWA, Shizue
; APPLICANT: HABASHITA, Junko
; APPLICANT: TAKETOMI, Shigehisa
; TITLE OF INVENTION: PARATHYROID HORMONE DERIVATIVES AND THEIR USE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/044,536A
; FILING DATE: 19-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/662,871
; FILING DATE: 12-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: CONLIN, David G
; REGISTRATION NUMBER: 27,026
; REFERENCE/DOCKET NUMBER: 46509-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids

```

; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: partial peptide
; LOCATION: 1..34
US-09-044-536A-10

Query Match 67.6%; Score 23; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.4e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
| | | | | | | | | | | | | | | | | | | | | |
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 25

US-09-044-536A-11

; Sequence 11, Application US/09044536A

; Patent No. 6025467

; GENERAL INFORMATION:

; APPLICANT: FUKUDA, Tsunehiko

; APPLICANT: NAKAGAWA, Shizue

; APPLICANT: HABASHITA, Junko

; APPLICANT: TAKETOMI, Shigehisa

; TITLE OF INVENTION: PARATHYROID HORMONE DERIVATIVES AND THEIR USE

; NUMBER OF SEQUENCES: 36

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN

; STREET: 130 Water Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: US

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/044,536A

; FILING DATE: 19-MAR-1998

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/662,871

; FILING DATE: 12-JUN-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: CONLIN, David G

; REGISTRATION NUMBER: 27,026

; REFERENCE/DOCKET NUMBER: 46509-DIV

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617)523-3400

; TELEFAX: (617)523-6440

; INFORMATION FOR SEQ ID NO: 11:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 34 amino acids


```

; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: partial peptide
; LOCATION: 1..34
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 11
; OTHER INFORMATION: /product= "Xaa-Ala(2-Naph)"
US-09-044-536A-12

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Query Match          67.6%; Score 23; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.4e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      12 GKHLNSMERVEWLRKKLQDVHNF 34
        |||||
Db      12 GKHLNSMERVEWLRKKLQDVHNF 34

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RESULT 27

US-09-044-536A-13

```

; Sequence 13, Application US/09044536A
; Patent No. 6025467

```

GENERAL INFORMATION:

```

; APPLICANT: FUKUDA, Tsunehiko
; APPLICANT: NAKAGAWA, Shizue
; APPLICANT: HABASHITA, Junko
; APPLICANT: TAKETOMI, Shigehisa
; TITLE OF INVENTION: PARATHYROID HORMONE DERIVATIVES AND THEIR USE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109

```

COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

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CURRENT APPLICATION DATA:

```

; APPLICATION NUMBER: US/09/044,536A
; FILING DATE: 19-MAR-1998

```

PRIOR APPLICATION DATA:

```

; APPLICATION NUMBER: 08/662,871
; FILING DATE: 12-JUN-1996

```

ATTORNEY/AGENT INFORMATION:

```

; NAME: CONLIN, David G
; REGISTRATION NUMBER: 27,026
; REFERENCE/DOCKET NUMBER: 46509-DIV

```

TELECOMMUNICATION INFORMATION:

```

; TELEPHONE: (617)523-3400

```


; TELEFAX: (617) 523-6440
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: partial peptide
; LOCATION: 1..34
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 10
; OTHER INFORMATION: /product= "Xaa=4-carboxyglutamic
; OTHER INFORMATION: acid"
US-09-044-536A-13

Query Match 67.6%; Score 23; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.4e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 28

US-09-044-536A-14

; Sequence 14, Application US/09044536A
; Patent No. 6025467
; GENERAL INFORMATION:
; APPLICANT: FUKUDA, Tsunehiko
; APPLICANT: NAKAGAWA, Shizue
; APPLICANT: HABASHITA, Junko
; APPLICANT: TAKETOMI, Shigehisa
; TITLE OF INVENTION: PARATHYROID HORMONE DERIVATIVES AND THEIR USE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/044,536A
; FILING DATE: 19-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/662,871
; FILING DATE: 12-JUN-1996
; ATTORNEY/AGENT INFORMATION:

; NAME: CONLIN, David G
 ; REGISTRATION NUMBER: 27,026
 ; REFERENCE/DOCKET NUMBER: 46509-DIV
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617)523-3400
 ; TELEFAX: (617)523-6440
 ; INFORMATION FOR SEQ ID NO: 14:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 34 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; FEATURE:
 ; NAME/KEY: partial peptide
 ; LOCATION: 1..34
 ; FEATURE:
 ; NAME/KEY: Modified-site
 ; LOCATION: 10
 ; OTHER INFORMATION: /product= "Xaa=2-aminosuberic acid"
 US-09-044-536A-14

Query Match 67.6%; Score 23; DB 3; Length 34;
 Best Local Similarity 100.0%; Pred. No. 1.4e-15;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 29

US-09-044-536A-15
 ; Sequence 15, Application US/09044536A
 ; Patent No. 6025467
 ; GENERAL INFORMATION:
 ; APPLICANT: FUKUDA, Tsunehiko
 ; APPLICANT: NAKAGAWA, Shizue
 ; APPLICANT: HABASHITA, Junko
 ; APPLICANT: TAKETOMI, Shigehisa
 ; TITLE OF INVENTION: PARATHYROID HORMONE DERIVATIVES AND THEIR USE
 ; NUMBER OF SEQUENCES: 36
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
 ; STREET: 130 Water Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: US
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/044,536A
 ; FILING DATE: 19-MAR-1998

```

; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/662,871
;   FILING DATE: 12-JUN-1996
; ATTORNEY/AGENT INFORMATION:
;   NAME: CONLIN, David G
;   REGISTRATION NUMBER: 27,026
;   REFERENCE/DOCKET NUMBER: 46509-DIV
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (617)523-3400
;   TELEFAX: (617)523-6440
; INFORMATION FOR SEQ ID NO: 15:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 34 amino acids
;     TYPE: amino acid
;     STRANDEDNESS:
;     TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
;   NAME/KEY: partial peptide
;   LOCATION: 1..34
; FEATURE:
;   NAME/KEY: Modified-site
;   LOCATION: 10
; OTHER INFORMATION: /product= "2-aminoadipic acid"
US-09-044-536A-15

```

```

Query Match          67.6%; Score 23; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.4e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      12 GKHLNSMERVEWLRKKLQDVHNF 34
        ||||||||||||||||||||
Db      12 GKHLNSMERVEWLRKKLQDVHNF 34

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RESULT 30

US-08-904-760B-22

```

; Sequence 22, Application US/08904760B
; Patent No. 6110892
; GENERAL INFORMATION:
;   APPLICANT: Jean-Rene, Barbier
;   APPLICANT: Neugebauer, Witold
;   APPLICANT: Ross, Virginia
;   APPLICANT: Whitfield, James
;   APPLICANT: Willick, Gordon E.
; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES FOR THE
; TITLE OF INVENTION: TREATMENT OF OSTEOPOROSIS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: NIXON & VANDERHYE P.C.
;   STREET: 1100 No. 6110892th Glebe Rd. 8th floor
;   CITY: Arlington
;   STATE: VA
;   COUNTRY: USA
;   ZIP: 22201-4741
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/904,760B
; FILING DATE: 01-AUG-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/691,647
; FILING DATE: 02-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Crawford, Arthur R.
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 1339-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-904-760B-22

```

```

Query Match          67.6%; Score 23; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.4e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      12 GKHLNSMERVEWLRKKLQDVHNF 34
        ||||||||||||||||||||
Db      12 GKHLNSMERVEWLRKKLQDVHNF 34

```

RESULT 31

US-09-108-661-13

; Sequence 13, Application US/09108661

; Patent No. 6287806

; GENERAL INFORMATION:

```

; APPLICANT: NISHIMURA, Osamu
; APPLICANT: KURIYAMA, Masato
; APPLICANT: KOYAMA, No. 6287806uyuki
; APPLICANT: FUKUDA, Tsunehiko
; TITLE OF INVENTION: METHOD FOR PRODUCING A BIOLOGICALLY
; TITLE OF INVENTION: ACTIVE RECOMBINANT CYSTEINE-FREE
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible

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; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/108,661
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/350,709
; FILING DATE: 07-DEC-1994
; APPLICATION NUMBER: 07/838,857
; FILING DATE: 18-FEB-1992
; APPLICATION NUMBER: JP 024841
; FILING DATE: 19-FEB-1991
; APPLICATION NUMBER: JP 0271438
; FILING DATE: 18-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: DAVID, RESNICK S
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 41614-FWC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX: 200291 STRE
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
US-09-108-661-13

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Query Match          67.6%; Score 23; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.4e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Qy      12 GKHLNSMERVEWLRKKLQDVHNF 34
        |||||
Db      12 GKHLNSMERVEWLRKKLQDVHNF 34

```

RESULT 32

US-09-007-466-6

; Sequence 6, Application US/09007466

; Patent No. 6313092

; GENERAL INFORMATION:

; APPLICANT: HOLLADAY, LESLIE A.

; APPLICANT: OLDENBURG, KEVIN R.

; TITLE OF INVENTION: METHOD FOR INCREASING THE

; TITLE OF INVENTION: ELECTROTRANSPORT FLUX OF POLYPEPTIDES

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: ALZA CORPORATION

; STREET: 950 PAGE MILL ROAD
 ; CITY: PALO ALTO
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 94303-0802
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/007,466
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/468,275
 ; FILING DATE: 06-JUN-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: MILLER, D. BYRON
 ; REGISTRATION NUMBER: 30,661
 ; REFERENCE/DOCKET NUMBER: 0360-0002; ARC-2349
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 496-8150
 ; TELEFAX: (415) 496-8048
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 34 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-09-007-466-6

Query Match 67.6%; Score 23; DB 4; Length 34;
 Best Local Similarity 100.0%; Pred. No. 1.4e-15;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 33

US-09-406-813-1

; Sequence 1, Application US/09406813
 ; Patent No. 6316410
 ; GENERAL INFORMATION:
 ; APPLICANT: Barbier, Jean-Rene
 ; APPLICANT: Morley, Paul
 ; APPLICANT: Whitfield, James
 ; APPLICANT: Willick, Gordon E.
 ; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES FOR THE TREATMENT OF
 ; TITLE OF INVENTION: OSTEOPOROSIS
 ; FILE REFERENCE: 10688-1B
 ; CURRENT APPLICATION NUMBER: US/09/406,813
 ; CURRENT FILING DATE: 1999-09-22
 ; PRIOR APPLICATION NUMBER: 08/904,760

; PRIOR FILING DATE: 1997-08-01
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-406-813-1

Query Match 67.6%; Score 23; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.4e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 34

US-08-952-980B-6

; Sequence 6, Application US/08952980B
; Patent No. 6333189
; GENERAL INFORMATION:
; APPLICANT: HOLLADAY, LESLIE A.
; APPLICANT: OLDENBURG, KEVIN R.
; TITLE OF INVENTION: METHOD FOR INCREASING THE
; TITLE OF INVENTION: ELECTROTRANSPORT FLUX OF POLYPEPTIDES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ALZA CORPORATION
; STREET: 950 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94303-0802
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/952,980B
; FILING DATE: 20-NOV-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: MILLER, D. BYRON
; REGISTRATION NUMBER: 30,661
; REFERENCE/DOCKET NUMBER: 2349 CIP 1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 496-8150
; TELEFAX: (650) 496-8048
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: protein
US-08-952-980B-6

Query Match 67.6%; Score 23; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.4e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 35

US-09-228-990-1

; Sequence 1, Application US/09228990

; Patent No. 6472505

: GENERAL INFORMATION:

APPLICANT: Condon, Stephen M.

APPLICANT: Morize, Isabelle

TITLE OF INVENTION: PEPTIDE PARATHYROID HORMONE ANALOGS

: NUMBER OF SEQUENCES: 88

CORRESPONDENCE ADDRESS:

ADDRESSEE: Rhone-Poulenc Rorer Inc.

; STREET: 500 Arcola Road, Mailstop 3C43

CITY: Collegeville

STATE: PA

COUNTRY: USA

ZIP: 19426

: COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

```
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
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```

; SOFTWARE: PatentIn Release #1.0, Version #1.30

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```

; CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/09/228,990

FILING DATE:

; CLASSIFICATION:

: PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/046,472

FILING DATE: 14-MAY-1997

: ATTORNEY/AGENT INFORMATION:

NAME: Martin Esq., Michael B.

; REGISTRATION NUMBER: 37,521

REFERENCE/DOCKET NUMBER: A2678B-WO

TELECOMMUNICATION INFORMATION:

TELEPHONE: (610) 454-2793

; TELEFAX: (610) 454-3808

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; INFORMATION FOR SEQ ID NO: 1:
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; SEQUENCE CHARACTERISTICS:

; LENGTH: 34 amino acids

TYPE: amino acid

; STRANDEDNESS:

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:
:      TOPOLOGY:  not relevant

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MOLECULE TYPE: peptide

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;    FRAGMENT TYPE:  N-terminal
```

US-09-228-990-1

Query Match 67.6%; Score 23; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.4e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 36

US-09-447-800-1

; Sequence 1, Application US/09447800
; Patent No. 6537965
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: ANALOGS
; FILE REFERENCE: 0609.4630001
; CURRENT APPLICATION NUMBER: US/09/447,800
; CURRENT FILING DATE: 1999-11-23
; EARLIER APPLICATION NUMBER: 60/110,152
; EARLIER FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (1)
; OTHER INFORMATION: Can be desamino Ser, desamino Ala, or desamino Gly
US-09-447-800-1

Query Match 67.6%; Score 23; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.4e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 37

US-09-447-800-2

; Sequence 2, Application US/09447800
; Patent No. 6537965
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: ANALOGS
; FILE REFERENCE: 0609.4630001
; CURRENT APPLICATION NUMBER: US/09/447,800

; CURRENT FILING DATE: 1999-11-23
; EARLIER APPLICATION NUMBER: 60/110,152
; EARLIER FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Desamino Gly
US-09-447-800-2

Query Match 67.6%; Score 23; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.4e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
| | | | | | | | | | | | | | | | | | | | | |
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 38
US-09-447-800-5
; Sequence 5, Application US/09447800
; Patent No. 6537965
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: ANALOGS
; FILE REFERENCE: 0609.4630001
; CURRENT APPLICATION NUMBER: US/09/447,800
; CURRENT FILING DATE: 1999-11-23
; EARLIER APPLICATION NUMBER: 60/110,152
; EARLIER FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Desamino Ala
US-09-447-800-5

Query Match 67.6%; Score 23; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.4e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
| | | | | | | | | | | | | | | | | | | | | |

Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 39

US-09-447-800-8

; Sequence 8, Application US/09447800
; Patent No. 6537965
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: ANALOGS
; FILE REFERENCE: 0609.4630001
; CURRENT APPLICATION NUMBER: US/09/447,800
; CURRENT FILING DATE: 1999-11-23
; EARLIER APPLICATION NUMBER: 60/110,152
; EARLIER FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Desamino Ser
US-09-447-800-8

Query Match 67.6%; Score 23; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.4e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 40

US-09-536-785A-22

; Sequence 22, Application US/09536785A
; Patent No. 6541450
; GENERAL INFORMATION:
; APPLICANT: BARBIER, JEAN-RENE
; APPLICANT: MORLEY, PAUL
; APPLICANT: NEUGEBAUER, WITOLD
; APPLICANT: ROSS, VIRGINIA J.S.
; APPLICANT: WHITFIELD, JAMES F.
; APPLICANT: WILLICK, GORDON E.
; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES FOR THE TREATMENT OF
; TITLE OF INVENTION: OSTEOPOROSIS
; FILE REFERENCE: 1339-9
; CURRENT APPLICATION NUMBER: US/09/536,785A
; CURRENT FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 08/904,760
; PRIOR FILING DATE: 1997-08-01

; PRIOR APPLICATION NUMBER: 08/691,647
; PRIOR FILING DATE: 1996-08-02
; PRIOR APPLICATION NUMBER: 08/262,495
; PRIOR FILING DATE: 1994-06-20
; PRIOR APPLICATION NUMBER: 60/040,560
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-536-785A-22

Query Match 67.6%; Score 23; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.4e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

Search completed: January 14, 2004, 10:43:29
Job time : 12.5452 secs

OM protein - protein search, using sw model

Run on: January 14, 2004, 10:28:19 ; Search time 10.0623 Seconds
(without alignments)
324.949 Million cell updates/sec

Title: US-09-843-221A-162
Perfect score: 34
Sequence: 1 SVSEIQLMHNRGKHLNSMERVEWLRKKLQDVHNF 34

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3709

Minimum DB seq length: 28
Maximum DB seq length: 40

Post-processing: Listing first 1000 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query	Match Length			
1	5	14.7	34	2	A84241	hypothetical prote
2	5	14.7	34	2	B97032	transcription regu
3	5	14.7	35	2	E95098	hypothetical prote
4	4	11.8	28	2	T09594	gene LFY protein -
5	4	11.8	29	1	A55527	pyrroloquinoline q
6	4	11.8	29	2	S01614	dystrophin - rat (
7	4	11.8	29	2	I78537	copper transportin
8	4	11.8	29	2	S78412	ribosomal protein
9	4	11.8	30	2	S63531	hypothetical prote
10	4	11.8	31	2	S44471	glucagon G1 - Nort
11	4	11.8	31	2	S44472	glucagon G2 - Nort
12	4	11.8	31	2	D70236	hypothetical prote
13	4	11.8	32	2	F23454	ovalbumin phosphos

14	4	11.8	32	2	D31461	T-cell receptor de
15	4	11.8	32	2	G84161	hypothetical prote
16	4	11.8	33	2	E81714	hypothetical prote
17	4	11.8	35	2	D23454	ovalbumin phosphos
18	4	11.8	35	2	G23454	ovalbumin phosphos
19	4	11.8	35	2	D82125	hypothetical prote
20	4	11.8	36	2	S70806	hypothetical prote
21	4	11.8	36	2	F95057	hypothetical prote
22	4	11.8	36	2	A84774	hypothetical prote
23	4	11.8	36	2	S46227	hypothetical prote
24	4	11.8	37	2	B60963	charybdotoxin 2 -
25	4	11.8	37	2	S71912	hemoglobin, extrac
26	4	11.8	37	2	T12635	homeotic protein H
27	4	11.8	39	1	CKFHCS	sarcotoxin IC - fl
28	4	11.8	39	2	S71913	hemoglobin, extrac
29	4	11.8	39	2	S77164	ycf32 protein - Sy
30	3	8.8	28	2	A42272	brain-type creatin
31	3	8.8	28	2	C32416	phospholipase A2 (
32	3	8.8	28	2	B60071	vasoactive intesti
33	3	8.8	28	2	A60304	vasoactive intesti
34	3	8.8	28	2	S58386	T-cell receptor be
35	3	8.8	28	2	S56121	type I DNA methylt
36	3	8.8	28	2	S70894	hypothetical prote
37	3	8.8	28	2	S22469	hypothetical prote
38	3	8.8	28	2	S26254	rel protein - chic
39	3	8.8	28	2	I59477	antigen, T-cell re
40	3	8.8	28	2	F46522	T-cell receptor et
41	3	8.8	28	2	H85908	hypothetical prote
42	3	8.8	29	1	GCCB	glucagon - Chinch
43	3	8.8	29	2	S39968	probable hydro-lya
44	3	8.8	29	2	S17147	galanin - chicken
45	3	8.8	29	2	JH0699	omega-conotoxin MV
46	3	8.8	29	2	A58537	omega-conotoxin MV
47	3	8.8	29	2	T44245	ribosomal protein
48	3	8.8	29	2	A05272	gelsolin, cytosoli
49	3	8.8	29	2	B44101	calmodulin, vasoac
50	3	8.8	29	2	S42642	probable rhicadhes
51	3	8.8	29	2	A00774	3-oxoadipate enol-
52	3	8.8	29	2	I84189	cyclic AMP recepto
53	3	8.8	29	2	A35445	repY protein - Esc
54	3	8.8	29	2	S65747	CDP-paratose synth
55	3	8.8	29	2	S65748	CDP-paratose synth
56	3	8.8	29	2	B41476	probable antigen 2
57	3	8.8	29	2	T31443	cytochrome bc chai
58	3	8.8	29	2	F85570	hypothetical prote
59	3	8.8	29	2	I49732	NADH2 dehydrogenas
60	3	8.8	30	2	S40309	tyrosine 3-monooxy
61	3	8.8	30	2	C21897	ornithine carbamoy
62	3	8.8	30	2	A05315	pancreatic ribonuc
63	3	8.8	30	2	A61333	trypsin (EC 3.4.21
64	3	8.8	30	2	S21815	H+-exporting ATPas
65	3	8.8	30	2	A44912	cysteine proteinas
66	3	8.8	30	2	B61125	glucagon-like pept
67	3	8.8	30	2	C61125	glucagon-like pept
68	3	8.8	30	2	F32502	T-cell receptor de
69	3	8.8	30	2	PD0013	cAMP response elem
70	3	8.8	30	2	S11617	ribosomal protein

71	3	8.8	30	2	S21195	spectrin beta chain
72	3	8.8	30	2	PC4172	profilin - rat (fr
73	3	8.8	30	2	A34461	heat shock protein
74	3	8.8	30	2	A22977	delta-endotoxin -
75	3	8.8	30	2	S08565	ribulose-bisphosph
76	3	8.8	30	2	S30333	N-carbamoyl-D-amin
77	3	8.8	30	2	PQ0444	hypothetical prote
78	3	8.8	30	2	B95020	hypothetical prote
79	3	8.8	30	2	H95021	hypothetical prote
80	3	8.8	30	2	F87254	hypothetical prote
81	3	8.8	30	2	D72276	hypothetical prote
82	3	8.8	30	2	D70253	conserved hypothet
83	3	8.8	30	2	B70165	hypothetical prote
84	3	8.8	30	2	E82294	hypothetical prote
85	3	8.8	30	2	D82251	hypothetical prote
86	3	8.8	30	2	S72626	small-cell-variant
87	3	8.8	30	2	A35687	probable 39K inorg
88	3	8.8	30	2	A32946	trypsin-like serin
89	3	8.8	30	2	PL0155	glycoprotein - Atl
90	3	8.8	30	2	S65519	carcinoembryonic a
91	3	8.8	30	2	S34765	4-hydroxybutyryl-C
92	3	8.8	30	2	D81532	hypothetical prote
93	3	8.8	30	2	A48923	retrovirus-related
94	3	8.8	30	2	B56586	storage hexamer 2
95	3	8.8	30	2	F81360	very hypothetical
96	3	8.8	30	2	S15650	NADH2 dehydrogenas
97	3	8.8	30	2	H97596	hypothetical prote
98	3	8.8	30	4	I52605	hypothetical MLL/E
99	3	8.8	31	2	T44925	hypothetical prote
100	3	8.8	31	2	S39019	glucagon-like pept
101	3	8.8	31	2	A58793	relaxin chain B -
102	3	8.8	31	2	A58586	conotoxin MrVIA -
103	3	8.8	31	2	F30608	Ig kappa chain V-I
104	3	8.8	31	2	D30608	Ig kappa chain V-I
105	3	8.8	31	2	F31461	T-cell receptor de
106	3	8.8	31	2	S03295	Ig alpha chain C r
107	3	8.8	31	2	S03297	Ig alpha chain C r
108	3	8.8	31	2	I52232	tau protein - huma
109	3	8.8	31	2	A36162	neutrophil-activat
110	3	8.8	31	2	S04980	ferritin heavy cha
111	3	8.8	31	2	S32610	antiviral protein
112	3	8.8	31	2	S38881	inner membrane pro
113	3	8.8	31	2	G95018	hypothetical prote
114	3	8.8	31	2	G95022	hypothetical prote
115	3	8.8	31	2	A95085	hypothetical prote
116	3	8.8	31	2	H95093	hypothetical prote
117	3	8.8	31	2	E95151	hypothetical prote
118	3	8.8	31	2	E87331	hypothetical prote
119	3	8.8	31	2	S14615	hypothetical prote
120	3	8.8	31	2	E70202	hypothetical prote
121	3	8.8	31	2	E70223	hypothetical prote
122	3	8.8	31	2	H70225	hypothetical prote
123	3	8.8	31	2	C70240	hypothetical prote
124	3	8.8	31	2	H70252	hypothetical prote
125	3	8.8	31	2	S49191	hypothetical prote
126	3	8.8	31	2	H82353	hypothetical prote
127	3	8.8	31	2	A05051	hypothetical prote

128	3	8.8	31	2	B23605	histone H1.3 - whe
129	3	8.8	31	2	S78738	protein YOL038c-a
130	3	8.8	31	2	A36221	cecropin P1 - pig
131	3	8.8	31	2	S27112	sarcosine - rabbi
132	3	8.8	31	2	C84082	hypothetical prote
133	3	8.8	31	2	D81591	hypothetical prote
134	3	8.8	31	2	G81558	hypothetical prote
135	3	8.8	31	2	G82816	hypothetical prote
136	3	8.8	31	2	F82565	hypothetical prote
137	3	8.8	32	1	TCEE	calcitonin - Japan
138	3	8.8	32	1	TCON2	calcitonin 2 - soc
139	3	8.8	32	1	TCON2C	calcitonin 2 - chu
140	3	8.8	32	1	TCON2P	calcitonin 2 - pin
141	3	8.8	32	1	TCON3	calcitonin 3 - coh
142	3	8.8	32	1	LFECI	ilvGMDA operon le
143	3	8.8	32	1	LFEBIT	ilvGEDA leader pep
144	3	8.8	32	2	S20719	alcohol dehydrogen
145	3	8.8	32	2	A61143	trypsin (EC 3.4.21
146	3	8.8	32	2	D32502	T-cell receptor de
147	3	8.8	32	2	A32502	T-cell receptor de
148	3	8.8	32	2	B40186	ubiquitin / riboso
149	3	8.8	32	2	S57780	histone H3 - rice
150	3	8.8	32	2	S51524	anchoring CII - bov
151	3	8.8	32	2	S36809	GTP-binding regula
152	3	8.8	32	2	A29743	translation initia
153	3	8.8	32	2	A59156	gliadin omega-5 -
154	3	8.8	32	2	A03367	lectin - Macrotylo
155	3	8.8	32	2	A44900	fimbrin, SEF 21 -
156	3	8.8	32	2	E91216	ilvGEDA operon lea
157	3	8.8	32	2	F86062	ilvGMDA operon le
158	3	8.8	32	2	AG0924	ilvGMDA operon at
159	3	8.8	32	2	S03273	photosystem II oxy
160	3	8.8	32	2	S08482	regulatory protein
161	3	8.8	32	2	E87694	hypothetical prote
162	3	8.8	32	2	D70222	hypothetical prote
163	3	8.8	32	2	E70225	hypothetical prote
164	3	8.8	32	2	B70241	hypothetical prote
165	3	8.8	32	2	B70257	hypothetical prote
166	3	8.8	32	2	H81215	hypothetical prote
167	3	8.8	32	2	D82353	hypothetical prote
168	3	8.8	32	2	E82279	hypothetical prote
169	3	8.8	32	2	E82089	hypothetical prote
170	3	8.8	32	2	H82416	hypothetical prote
171	3	8.8	32	2	T17394	vrlN protein - Dic
172	3	8.8	32	2	S23476	hypothetical prote
173	3	8.8	32	2	S22304	hypothetical prote
174	3	8.8	32	2	S78323	photosystem II pro
175	3	8.8	32	2	I38619	zinc finger protei
176	3	8.8	32	2	S28398	t-complex protein
177	3	8.8	32	2	T14569	hypothetical prote
178	3	8.8	32	2	H84081	hypothetical prote
179	3	8.8	32	2	F82833	hypothetical prote
180	3	8.8	32	2	JC5802	ovulation stimulat
181	3	8.8	32	2	E85588	hypothetical prote
182	3	8.8	33	2	D21897	ornithine carbamoy
183	3	8.8	33	2	S43312	2',3'-cyclic-nucle
184	3	8.8	33	2	S26859	chitinase (EC 3.2.

185	3	8.8	33	2	I52219	c-ras-Ki-2 protein
186	3	8.8	33	2	I53221	K-ras protein - hu
187	3	8.8	33	2	E32502	T-cell receptor de
188	3	8.8	33	2	A31461	T-cell receptor de
189	3	8.8	33	2	B31461	T-cell receptor de
190	3	8.8	33	2	A03150	retinoic acid-bind
191	3	8.8	33	2	C46027	neurotransmitter t
192	3	8.8	33	2	PQ0150	dnaK-type molecula
193	3	8.8	33	2	B44906	L1 protein - human
194	3	8.8	33	2	PQ0418	matrix protein M1
195	3	8.8	33	2	S34505	hypothetical prote
196	3	8.8	33	2	G95006	hypothetical prote
197	3	8.8	33	2	C95200	hypothetical prote
198	3	8.8	33	2	F84163	hypothetical prote
199	3	8.8	33	2	H82475	hypothetical prote
200	3	8.8	33	2	S68096	lactate dehydrogen
201	3	8.8	33	2	E82526	hypothetical prote
202	3	8.8	33	2	G85600	hypothetical prote
203	3	8.8	33	2	H85651	hypothetical prote
204	3	8.8	33	2	AC1012	hypothetical prote
205	3	8.8	33	2	C97406	hypothetical prote
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207	3	8.8	34	2	A40298	dermaseptin - Sauv
208	3	8.8	34	2	JS0426	big gastrin - goat
209	3	8.8	34	2	I48887	cryptdin-4 - mouse
210	3	8.8	34	2	I32502	T-cell receptor de
211	3	8.8	34	2	H31461	T-cell receptor de
212	3	8.8	34	2	A19197	class II histocomp
213	3	8.8	34	2	D48147	troponin I (altern
214	3	8.8	34	2	A43564	neurogenic protein
215	3	8.8	34	2	H95047	hypothetical prote
216	3	8.8	34	2	D95189	hypothetical prote
217	3	8.8	34	2	C90973	hypothetical prote
218	3	8.8	34	2	F70242	hypothetical prote
219	3	8.8	34	2	B70252	hypothetical prote
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221	3	8.8	34	2	F81919	hypothetical prote
222	3	8.8	34	2	F81044	hypothetical prote
223	3	8.8	34	2	F82163	hypothetical prote
224	3	8.8	34	2	E82100	hypothetical prote
225	3	8.8	34	2	A82048	hypothetical prote
226	3	8.8	34	2	B82449	hypothetical prote
227	3	8.8	34	2	S13662	cellulase (EC 3.2.
228	3	8.8	34	2	A60110	repetitive protein
229	3	8.8	34	2	S44828	F54F2.3 protein -
230	3	8.8	34	2	S68648	major glycoprotein
231	3	8.8	34	2	S40662	P-cadherin - mouse
232	3	8.8	34	2	F84079	hypothetical prote
233	3	8.8	34	2	H81600	hypothetical prote
234	3	8.8	34	2	H82820	hypothetical prote
235	3	8.8	34	2	C82819	hypothetical prote
236	3	8.8	34	2	C82764	hypothetical prote
237	3	8.8	34	2	B82679	hypothetical prote
238	3	8.8	34	2	G85820	unknown protein en
239	3	8.8	34	2	S12554	hydroxymethylgluta
240	3	8.8	35	1	NTSRPM	neurotoxin P2 - sc
241	3	8.8	35	2	E38601	Ig kappa chain V r

242	3	8.8	35	2	S20766	Ig heavy chain V r
243	3	8.8	35	2	A05302	hemoglobin beta ch
244	3	8.8	35	2	A29663	histone H4 - starf
245	3	8.8	35	2	S27154	ribosomal protein
246	3	8.8	35	2	S13435	lectin III - furze
247	3	8.8	35	2	S18224	filamentous hemagg
248	3	8.8	35	2	S18226	opacity protein op
249	3	8.8	35	2	T07870	major latex protei
250	3	8.8	35	2	B33770	hypothetical prote
251	3	8.8	35	2	PS0439	potassium channel
252	3	8.8	35	2	I48925	homeobox protein -
253	3	8.8	35	2	F87622	hypothetical prote
254	3	8.8	35	2	C96619	protein T30E16.7 [
255	3	8.8	35	2	B84674	hypothetical prote
256	3	8.8	35	2	F84395	hypothetical prote
257	3	8.8	35	2	B82012	hypothetical prote
258	3	8.8	35	2	H81948	hypothetical prote
259	3	8.8	35	2	A82151	hypothetical prote
260	3	8.8	35	2	F82051	hypothetical prote
261	3	8.8	35	2	I64003	hypothetical prote
262	3	8.8	35	2	F69827	hypothetical prote
263	3	8.8	35	2	C69977	hypothetical prote
264	3	8.8	35	2	S65772	early nodulin 40 -
265	3	8.8	35	2	G60529	hemocyanin M3' - c
266	3	8.8	35	2	A60959	agelenin - funnel-
267	3	8.8	35	2	S49309	oncofetal protein
268	3	8.8	35	2	C81560	hypothetical prote
269	3	8.8	35	2	A85660	hypothetical prote
270	3	8.8	35	2	B85708	unknown protein en
271	3	8.8	35	2	AE0612	hypothetical prote
272	3	8.8	36	1	A48850	chloride channel 1
273	3	8.8	36	2	JN0402	insect toxin II -
274	3	8.8	36	2	H32502	T-cell receptor de
275	3	8.8	36	2	C32502	T-cell receptor de
276	3	8.8	36	2	S08552	ribosomal protein
277	3	8.8	36	2	S72299	ribosomal protein
278	3	8.8	36	2	I46593	myosin - pig (frag
279	3	8.8	36	2	B31872	retinoic acid-bind
280	3	8.8	36	2	S35572	zona pellucida pro
281	3	8.8	36	2	B41481	virulence-associat
282	3	8.8	36	2	A38659	methanol dehydroge
283	3	8.8	36	2	E84416	hypothetical prote
284	3	8.8	36	2	S17834	acetyl-CoA carboxy
285	3	8.8	36	2	E70220	hypothetical prote
286	3	8.8	36	2	E70238	hypothetical prote
287	3	8.8	36	2	F64604	hypothetical prote
288	3	8.8	36	2	G81853	hypothetical prote
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291	3	8.8	36	2	A82163	hypothetical prote
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293	3	8.8	36	2	A82092	hypothetical prote
294	3	8.8	36	2	B82093	hypothetical prote
295	3	8.8	36	2	A82437	hypothetical prote
296	3	8.8	36	2	A69326	hypothetical prote
297	3	8.8	36	2	S67795	probable membrane
298	3	8.8	36	2	T22263	hypothetical prote

299	3	8.8	36	2	S66282	defensin beta-1 -
300	3	8.8	36	2	A57443	guanylate cyclase
301	3	8.8	36	2	D83682	hypothetical prote
302	3	8.8	36	2	F84074	hypothetical prote
303	3	8.8	36	2	A56634	neuropeptide F - A
304	3	8.8	36	2	S77071	probable plastoqui
305	3	8.8	36	2	AF1015	hypothetical prote
306	3	8.8	36	2	AI1841	hypothetical prote
307	3	8.8	37	1	S32792	iberiotoxin - east
308	3	8.8	37	1	HSWT93	histone H2A.3 - wh
309	3	8.8	37	1	R5BS36	ribosomal protein
310	3	8.8	37	2	S48656	fusicoccin recepto
311	3	8.8	37	2	S03570	trypsin (EC 3.4.21
312	3	8.8	37	2	S39367	proteinase omega -
313	3	8.8	37	2	S06217	transforming prote
314	3	8.8	37	2	A60963	charybdotoxin 1 [v
315	3	8.8	37	2	A30607	Ig kappa chain V-I
316	3	8.8	37	2	PC1121	antifungal 25K pro
317	3	8.8	37	2	G01887	MEK kinase - human
318	3	8.8	37	2	S07517	gene 6.3 protein -
319	3	8.8	37	2	E70241	hypothetical prote
320	3	8.8	37	2	D83199	hypothetical prote
321	3	8.8	37	2	H82304	hypothetical prote
322	3	8.8	37	2	S21132	photosystem II cyt
323	3	8.8	37	2	F59103	hypothetical prote
324	3	8.8	37	2	T36662	small hypothetical
325	3	8.8	37	2	T11815	hypothetical prote
326	3	8.8	37	2	A57127	diuretic hormone 1
327	3	8.8	37	2	C32112	R15 gamma peptide
328	3	8.8	37	2	S68261	hypothetical prote
329	3	8.8	37	2	S49982	Tcell receptor alp
330	3	8.8	37	2	B39030	androgen-binding p
331	3	8.8	37	2	PN0550	metabotropic gluta
332	3	8.8	37	2	S70931	histone-like prote
333	3	8.8	37	2	F81403	hypothetical prote
334	3	8.8	37	2	AH0844	hypothetical prote
335	3	8.8	38	1	R5EC36	ribosomal protein
336	3	8.8	38	2	C34047	stylar glycoprotei
337	3	8.8	38	2	T11763	acetyl-CoA carboxy
338	3	8.8	38	2	S39034	lipid transfer pro
339	3	8.8	38	2	PS0129	H-2 class I histoc
340	3	8.8	38	2	S50764	ribosomal protein
341	3	8.8	38	2	E72247	ribosomal protein
342	3	8.8	38	2	H83113	50S ribosomal prot
343	3	8.8	38	2	AG0028	50S ribosomal prot
344	3	8.8	38	2	D91149	50S ribosomal subu
345	3	8.8	38	2	AF1008	50S ribosomal chai
346	3	8.8	38	2	PH1920	annexin-like 40K p
347	3	8.8	38	2	S72344	pileE protein - Nei
348	3	8.8	38	2	A60216	hyperglycemic horm
349	3	8.8	38	2	S65416	pyruvate synthase
350	3	8.8	38	2	H91111	hypothetical prote
351	3	8.8	38	2	D90631	hypothetical prote
352	3	8.8	38	2	E72306	hypothetical prote
353	3	8.8	38	2	E81873	hypothetical prote
354	3	8.8	38	2	T14885	hypothetical prote
355	3	8.8	38	2	A82478	hypothetical prote

356	3	8.8	38	2	E82463	hypothetical prote
357	3	8.8	38	2	A82450	hypothetical prote
358	3	8.8	38	2	D37842	hypothetical prote
359	3	8.8	38	2	B69492	hypothetical prote
360	3	8.8	38	2	S23173	photosystem I chai
361	3	8.8	38	2	S58601	hypothetical prote
362	3	8.8	38	2	T01741	hypothetical prote
363	3	8.8	38	2	B42087	mating factor a2 -
364	3	8.8	38	2	B39888	synapsin I - bovin
365	3	8.8	38	2	B49012	orf 5' of megl1 - m
366	3	8.8	38	2	A83863	hypothetical prote
367	3	8.8	38	2	H81603	hypothetical prote
368	3	8.8	38	2	E82858	hypothetical prote
369	3	8.8	38	2	G71305	probable ribosomal
370	3	8.8	38	2	B97327	hypothetical prote
371	3	8.8	38	2	H85994	50S ribosomal subu
372	3	8.8	38	2	T08652	hypothetical prote
373	3	8.8	38	2	AH0774	hypothetical prote
374	3	8.8	39	1	CTDFAS	corticotropin - sp
375	3	8.8	39	1	HWGH3Z	exendin-3 - Mexica
376	3	8.8	39	1	HWGH4G	exendin-4 - Gila m
377	3	8.8	39	2	B45946	gamma-glutamyltran
378	3	8.8	39	2	S09645	hygromycin-B kinas
379	3	8.8	39	2	A01458	corticotropin - fi
380	3	8.8	39	2	PN0127	corticotropin - se
381	3	8.8	39	2	A61127	adrenocorticotropi
382	3	8.8	39	2	A01459	corticotropin - os
383	3	8.8	39	2	A01457	corticotropin - ra
384	3	8.8	39	2	C55995	prostaglandin E2 r
385	3	8.8	39	2	PH0878	Ig kappa chain V r
386	3	8.8	39	2	S72459	ribosomal protein
387	3	8.8	39	2	PQ0011	tubulin beta chain
388	3	8.8	39	2	S63482	tubulin beta chain
389	3	8.8	39	2	A45793	actin - nematode (
390	3	8.8	39	2	AH2286	photosystem II pro
391	3	8.8	39	2	G64944	yebJ protein - Esc
392	3	8.8	39	2	A85795	hypothetical prote
393	3	8.8	39	2	S78008	fucosyltransferase
394	3	8.8	39	2	H95087	hypothetical prote
395	3	8.8	39	2	H95146	hypothetical prote
396	3	8.8	39	2	D70239	hypothetical prote
397	3	8.8	39	2	C70254	hypothetical prote
398	3	8.8	39	2	G81899	hypothetical prote
399	3	8.8	39	2	B81912	hypothetical prote
400	3	8.8	39	2	B81954	very hypothetical
401	3	8.8	39	2	F82329	hypothetical prote
402	3	8.8	39	2	A44918	lactococcin G pept
403	3	8.8	39	2	S73118	photosystem II pro
404	3	8.8	39	2	PC4294	high mobility grou
405	3	8.8	39	2	T15158	hypothetical prote
406	3	8.8	39	2	I46466	luteinizing hormon
407	3	8.8	39	2	B40984	finger protein zfe
408	3	8.8	39	2	T03365	gene e2 protein -
409	3	8.8	39	2	F81587	hypothetical prote
410	3	8.8	39	2	E81540	hypothetical prote
411	3	8.8	39	2	T12905	hypothetical prote
412	3	8.8	39	2	AD0162	hypothetical prote

413	3	8.8	39	2	AE3109	hypothetical prote
414	3	8.8	40	1	SWFGS	sauvagine - Sauvag
415	3	8.8	40	2	B61320	plastocyanin - Aqu
416	3	8.8	40	2	S52343	hypothetical prote
417	3	8.8	40	2	S00264	creatine kinase (E
418	3	8.8	40	2	S34407	adenylate kinase (
419	3	8.8	40	2	PQ0202	endo-1,4-beta-xyla
420	3	8.8	40	2	S50021	trypsin-like prote
421	3	8.8	40	2	B60908	beta-lactamase (EC
422	3	8.8	40	2	B41440	protein disulfide-
423	3	8.8	40	2	A19940	antithrombin III -
424	3	8.8	40	2	B59005	thymosin beta - sc
425	3	8.8	40	2	A59005	thymosin beta - se
426	3	8.8	40	2	JU0225	sapecin C - flesh
427	3	8.8	40	2	B31791	sarcotoxin ID - fl
428	3	8.8	40	2	S07969	T-cell receptor al
429	3	8.8	40	2	I50012	MHC class I protei
430	3	8.8	40	2	I50013	MHC class I protei
431	3	8.8	40	2	S61539	ribosomal protein
432	3	8.8	40	2	A60171	proteoglycan core
433	3	8.8	40	2	A60645	tubulin beta chain
434	3	8.8	40	2	A29184	vitellogenin - tur
435	3	8.8	40	2	S65907	conglutin gamma -
436	3	8.8	40	2	S08656	protein VI - human
437	3	8.8	40	2	A53708	indolepyruvate syn
438	3	8.8	40	2	T08107	nonenzymatic prote
439	3	8.8	40	2	S71917	hemoglobin, extrac
440	3	8.8	40	2	S58853	homeotic protein u
441	3	8.8	40	2	H95063	hypothetical prote
442	3	8.8	40	2	H91281	hypothetical prote
443	3	8.8	40	2	A87642	hypothetical prote
444	3	8.8	40	2	F87419	hypothetical prote
445	3	8.8	40	2	C32338	hypothetical 4K pr
446	3	8.8	40	2	C72398	hypothetical prote
447	3	8.8	40	2	D70237	hypothetical prote
448	3	8.8	40	2	S44935	hypothetical prote
449	3	8.8	40	2	A82203	hypothetical prote
450	3	8.8	40	2	G82484	hypothetical prote
451	3	8.8	40	2	A82382	hypothetical prote
452	3	8.8	40	2	I39944	regulatory extrace
453	3	8.8	40	2	F69677	phosphatase (RapK)
454	3	8.8	40	2	I41476	probable antigen 9
455	3	8.8	40	2	S27709	hypothetical prote
456	3	8.8	40	2	T11811	hypothetical prote
457	3	8.8	40	2	T07472	hypothetical prote
458	3	8.8	40	2	T07516	hypothetical prote
459	3	8.8	40	2	T07523	hypothetical prote
460	3	8.8	40	2	T07560	hypothetical prote
461	3	8.8	40	2	T07583	hypothetical prote
462	3	8.8	40	2	T48629	hypothetical prote
463	3	8.8	40	2	S53001	mitotic-specific c
464	3	8.8	40	2	T03831	hypothetical prote
465	3	8.8	40	2	A47753	beta-defensin-10 -
466	3	8.8	40	2	G45495	beta-defensin-7 -
467	3	8.8	40	2	I45495	beta-defensin-9 -
468	3	8.8	40	2	S56768	capsid protein - L
469	3	8.8	40	2	T07206	hypothetical prote

470	3	8.8	40	2	H81592	hypothetical prote
471	3	8.8	40	2	F81511	hypothetical prote
472	3	8.8	40	2	G82620	hypothetical prote
473	3	8.8	40	2	A82590	hypothetical prote
474	3	8.8	40	2	A86123	hypothetical prote
475	3	8.8	40	2	B97413	hypothetical prote
476	2	5.9	28	1	LFSEW	trp operon leader
477	2	5.9	28	1	LFEBLT	leu operon leader
478	2	5.9	28	1	LFECL	leu operon leader
479	2	5.9	28	1	G9BPSV	gene 9 protein - s
480	2	5.9	28	2	S41774	ubiquinol-cytochro
481	2	5.9	28	2	S71598	cytochrome P450 HP
482	2	5.9	28	2	S04341	cytochrome P450 PB
483	2	5.9	28	2	PX0033	cytochrome P450 te
484	2	5.9	28	2	S66436	allophycocyanin al
485	2	5.9	28	2	S47624	D-aspartate oxidas
486	2	5.9	28	2	T14210	NADH2 dehydrogenas
487	2	5.9	28	2	T14213	NADH2 dehydrogenas
488	2	5.9	28	2	T12301	NADH2 dehydrogenas
489	2	5.9	28	2	PC1162	cytochrome-c oxida
490	2	5.9	28	2	S21278	glutathione transf
491	2	5.9	28	2	C33948	glutathione transf
492	2	5.9	28	2	A34244	hexokinase (EC 2.7
493	2	5.9	28	2	D38578	protein kinase 4 (
494	2	5.9	28	2	B39116	epidermal growth f
495	2	5.9	28	2	A31859	deoxycytidine kina
496	2	5.9	28	2	B54257	deoxynucleoside ki
497	2	5.9	28	2	I55596	lysosomal acid lip
498	2	5.9	28	2	B35948	phospholipase A2 (
499	2	5.9	28	2	A35115	hypothetical prote
500	2	5.9	28	2	A61281	lysozyme homolog A
501	2	5.9	28	2	A61529	chymotrypsin (EC 3
502	2	5.9	28	2	A60291	24K proteinase (EC
503	2	5.9	28	2	S08186	proteasome beta ch
504	2	5.9	28	2	S55729	orotidine-5'-monop
505	2	5.9	28	2	I40034	trpE protein - Bac
506	2	5.9	28	2	A32643	deoxyribodipyrimid
507	2	5.9	28	2	S77854	glutamate-tRNA lig
508	2	5.9	28	2	JN0366	proteinase inhibit
509	2	5.9	28	2	JX0059	serine proteinase
510	2	5.9	28	2	S07156	trypsin inhibitor
511	2	5.9	28	2	JX0058	trypsin inhibitor
512	2	5.9	28	2	B45041	trypsin inhibitor
513	2	5.9	28	2	S20393	trypsin inhibitor
514	2	5.9	28	2	A25802	2S seed storage pr
515	2	5.9	28	2	T47196	RAS protein [impor
516	2	5.9	28	2	A61322	somatostatin-28 -
517	2	5.9	28	2	B60583	glycoprotein hormo
518	2	5.9	28	2	A38232	vasoactive intesti
519	2	5.9	28	2	A60303	vasoactive intesti
520	2	5.9	28	2	JT0412	bombyxin-IV chain
521	2	5.9	28	2	A56366	intestinal trefoil
522	2	5.9	28	2	C44180	alpha-neurotoxin-1
523	2	5.9	28	2	C39327	long neurotoxin -
524	2	5.9	28	2	I32529	Ig lambda chain V
525	2	5.9	28	2	PC1001	Ig light chain V r
526	2	5.9	28	2	B47719	T-cell receptor al

527	2	5.9	28	2	D47719	T-cell receptor al
528	2	5.9	28	2	S58389	T-cell receptor be
529	2	5.9	28	2	PH0250	T-cell receptor Vb
530	2	5.9	28	2	PH0247	T-cell receptor Vb
531	2	5.9	28	2	A49829	T-cell receptor va
532	2	5.9	28	2	D49829	T-cell receptor va
533	2	5.9	28	2	PH1908	T-cell receptor al
534	2	5.9	28	2	D41912	T-cell receptor be
535	2	5.9	28	2	G47719	house-dust-mite-re
536	2	5.9	28	2	E49533	T-cell receptor be
537	2	5.9	28	2	I46921	gene Bota protein
538	2	5.9	28	2	I56139	MHC class I HLA-J
539	2	5.9	28	2	S11618	ribosomal protein
540	2	5.9	28	2	S51060	ribosomal protein
541	2	5.9	28	2	S51067	ribosomal protein
542	2	5.9	28	2	S72460	ribosomal protein
543	2	5.9	28	2	S08569	ribosomal protein
544	2	5.9	28	2	S10052	ribosomal protein
545	2	5.9	28	2	I50169	alpha-1 type-1 col
546	2	5.9	28	2	S55442	beta A2 crystallin
547	2	5.9	28	2	A45626	beta 2-tubulin - n
548	2	5.9	28	2	S21231	calcium-binding pr
549	2	5.9	28	2	A23691	apolipoprotein C-I
550	2	5.9	28	2	A05296	fibrinogen alpha c
551	2	5.9	28	2	A61113	cellular retinol-b
552	2	5.9	28	2	B35577	cell adhesion rece
553	2	5.9	28	2	I48349	fibronectin - mous
554	2	5.9	28	2	A61233	retinol-binding pr
555	2	5.9	28	2	I45911	dnaK-type molecula
556	2	5.9	28	2	PQ0263	dnaK-type molecula
557	2	5.9	28	2	A03356	omega-gliadin - ei
558	2	5.9	28	2	A60359	pollen allergen DG
559	2	5.9	28	2	A60752	outer membrane pro
560	2	5.9	28	2	PQ0691	photosystem I 5.6K
561	2	5.9	28	2	G32351	34K class B flagel
562	2	5.9	28	2	S47614	zinc finger protei
563	2	5.9	28	2	S49924	stp protein (Baker
564	2	5.9	28	2	PN0047	signal transductio
565	2	5.9	28	2	B39227	calcium channel pr
566	2	5.9	28	2	F54346	pyruvate synthase
567	2	5.9	28	2	A36153	major allergen Ole
568	2	5.9	28	2	B54127	dolichyl-diphospho
569	2	5.9	28	2	S56746	alpha-synuclein, N
570	2	5.9	28	2	I48178	orphan receptor -
571	2	5.9	28	2	S29135	aminopyrine N-deme
572	2	5.9	28	2	S29136	aminopyrine N-deme
573	2	5.9	28	2	PN0625	homeobox JRX prote
574	2	5.9	28	2	B56779	tetM 5'-region lea
575	2	5.9	28	2	JU0297	fruR-shl operon le
576	2	5.9	28	2	G90638	leu operon leader
577	2	5.9	28	2	C90639	fruR leader peptid
578	2	5.9	28	2	B47310	MHVS28AA - murine
579	2	5.9	28	2	E64656	hypothetical prote
580	2	5.9	28	2	B64669	hypothetical prote
581	2	5.9	28	2	S15235	hypothetical prote
582	2	5.9	28	2	C56262	uvrB 3'-region hyp
583	2	5.9	28	2	E81239	hypothetical prote

584	2	5.9	28	2	I60364	phosphorybosylpyro
585	2	5.9	28	2	B39191	hypothetical prote
586	2	5.9	28	2	T17391	hypothetical prote
587	2	5.9	28	2	A56499	brevicin-27 - Lact
588	2	5.9	28	2	A41476	probable antigen 1
589	2	5.9	28	2	S16228	aryl acylamidase -
590	2	5.9	28	2	T37143	hypothetical prote
591	2	5.9	28	2	PS0106	2-phosphinomethylm
592	2	5.9	28	2	G69384	conserved hypothet
593	2	5.9	28	2	A69259	hypothetical prote
594	2	5.9	28	2	T06925	hypothetical prote
595	2	5.9	28	2	S38524	rRNA N-glycosidase
596	2	5.9	28	2	S21742	3-oxoacyl-[acyl-ca
597	2	5.9	28	2	PQ0800	calmodulin antagon
598	2	5.9	28	2	T06340	ribosomal protein
599	2	5.9	28	2	T07599	hypothetical prote
600	2	5.9	28	2	PH0220	peroxidase (EC 1.1
601	2	5.9	28	2	JQ0272	hypothetical 3K pr
602	2	5.9	28	2	S46250	fatty-acid-binding
603	2	5.9	28	2	A44923	carboxypeptidase 3
604	2	5.9	28	2	S64701	hypothetical prote
605	2	5.9	28	2	T38041	similarity to yeas
606	2	5.9	28	2	A60698	trichocyst protein
607	2	5.9	28	2	A27261	proteinase inhibit
608	2	5.9	28	2	A61417	bdellin B-3 - medi
609	2	5.9	28	2	S06668	toxin-like protein
610	2	5.9	28	2	S07826	venom protein - Am
611	2	5.9	28	2	C34923	omega-agatoxin IIA
612	2	5.9	28	2	A44877	cell surface prote
613	2	5.9	28	2	JW0019	mast cell degranul
614	2	5.9	28	2	A61273	interleukin-1 - st
615	2	5.9	28	2	S68643	nicotinic acetylch
616	2	5.9	28	2	PC2162	angiotensin II rec
617	2	5.9	28	2	I54183	cell adhesion regu
618	2	5.9	28	2	S54338	cytochrome P450 CY
619	2	5.9	28	2	I52627	erythrocyte chemok
620	2	5.9	28	2	JQ1035	hypothetical 3.2K
621	2	5.9	28	2	PH1335	Ig heavy chain DJ
622	2	5.9	28	2	S37683	protein IEF SSP 91
623	2	5.9	28	2	S37686	protein IEF SSP 92
624	2	5.9	28	2	PH1911	T-cell receptor al
625	2	5.9	28	2	I39288	ZF3 domain - human
626	2	5.9	28	2	PL0005	pepsin A (EC 3.4.2
627	2	5.9	28	2	A60692	proline-rich prote
628	2	5.9	28	2	PC2239	heat shock protein
629	2	5.9	28	2	PT0366	T-cell receptor be
630	2	5.9	28	2	I58115	cystic fibrosis tr
631	2	5.9	28	2	A46690	sialic acid-specif
632	2	5.9	28	2	C83797	hypothetical prote
633	2	5.9	28	2	C83969	hypothetical prote
634	2	5.9	28	2	S51593	myrB protein - Mic
635	2	5.9	28	2	C85490	fruR leader peptid
636	2	5.9	28	2	C97078	hypothetical prote
637	2	5.9	28	2	F97000	hypothetical prote
638	2	5.9	28	2	G85489	leu operon leader
639	2	5.9	28	2	AB1093	hypothetical prote
640	2	5.9	28	2	T06490	probable ribulose-

641	2	5.9	28	2	S73563	H ⁺ -transporting tw
642	2	5.9	28	2	AG0516	leu operon leader
643	2	5.9	28	4	I68614	frame shifted FMR1
644	2	5.9	28	4	JN0014	GABA(A) receptor a
645	2	5.9	29	1	TIPU	trypsin inhibitor
646	2	5.9	29	1	TIPU3	trypsin inhibitor
647	2	5.9	29	1	TIPU2B	trypsin inhibitor
648	2	5.9	29	1	GCOPV	glucagon - North A
649	2	5.9	29	1	GCDK	glucagon - duck
650	2	5.9	29	1	A61583	glucagon - ostrich
651	2	5.9	29	1	GCFLE	glucagon - Europea
652	2	5.9	29	1	GCDF	glucagon - smaller
653	2	5.9	29	1	GCEN	glucagon - elephan
654	2	5.9	29	1	GCTTS	glucagon - slider
655	2	5.9	29	1	TNLJBR	trans-activating t
656	2	5.9	29	1	Q1BP57	gene 1.5 protein -
657	2	5.9	29	2	A60558	cytochrome P450 HL
658	2	5.9	29	2	T17079	NADH2 dehydrogenas
659	2	5.9	29	2	A48427	flavoheмоglobin hm
660	2	5.9	29	2	A54234	cytochrome-c oxida
661	2	5.9	29	2	S08201	peroxidase (EC 1.1
662	2	5.9	29	2	A26208	acetyl-CoA C-acety
663	2	5.9	29	2	A22018	phosphotransferase
664	2	5.9	29	2	S46211	kallikrein rK8 (pK
665	2	5.9	29	2	S28174	heat-shock protein
666	2	5.9	29	2	A32414	bothrolysin (EC 3.
667	2	5.9	29	2	S17432	H ⁺ -transporting tw
668	2	5.9	29	2	S02578	H ⁺ -transporting tw
669	2	5.9	29	2	S23122	peptidylprolyl iso
670	2	5.9	29	2	JU0211	squash-type trypsi
671	2	5.9	29	2	T03653	phospholipid trans
672	2	5.9	29	2	C24536	alpha-amylase/tryp
673	2	5.9	29	2	C25310	alpha-amylase/tryp
674	2	5.9	29	2	D55998	brevinin-2Ed - edi
675	2	5.9	29	2	D53578	brevinin-2Ee - edi
676	2	5.9	29	2	A61509	islet amyloid poly
677	2	5.9	29	2	A91740	glucagon - turkey
678	2	5.9	29	2	A91741	glucagon - rabbit
679	2	5.9	29	2	A91742	glucagon - Arabian
680	2	5.9	29	2	S07211	glucagon - marbled
681	2	5.9	29	2	A61135	glucagon - bigeye
682	2	5.9	29	2	C39258	glucagon - common
683	2	5.9	29	2	C60840	glucagon I - Europ
684	2	5.9	29	2	S39018	glucagon - bowfin
685	2	5.9	29	2	A39462	cholestokinin - do
686	2	5.9	29	2	A60791	toxin II.9 - scorp
687	2	5.9	29	2	A43620	omega-conotoxin GV
688	2	5.9	29	2	B43620	omega-conotoxin GV
689	2	5.9	29	2	I52628	low affinity nerve
690	2	5.9	29	2	C61233	conceptus protein
691	2	5.9	29	2	S10061	Ig heavy chain (cl
692	2	5.9	29	2	PH1328	Ig heavy chain DJ
693	2	5.9	29	2	PH0239	T-cell receptor Vb
694	2	5.9	29	2	PH0251	T-cell receptor Vb
695	2	5.9	29	2	PH0254	T-cell receptor Vb
696	2	5.9	29	2	PH0233	T-cell receptor Vb
697	2	5.9	29	2	E31485	Ig heavy chain V r

698	2	5.9	29	2	H31485	Ig kappa chain V r
699	2	5.9	29	2	G31461	T-cell receptor de
700	2	5.9	29	2	C47719	T-cell receptor al
701	2	5.9	29	2	E47719	house-dust-mite-re
702	2	5.9	29	2	H47719	house-dust-mite-re
703	2	5.9	29	2	PS0134	H-2 class I histoc
704	2	5.9	29	2	PS0132	H-2 class I histoc
705	2	5.9	29	2	D32533	class II histocomp
706	2	5.9	29	2	I37534	gene HLA-DRB prote
707	2	5.9	29	2	I37535	gene HLA-DRB prote
708	2	5.9	29	2	I37536	MHC class II histo
709	2	5.9	29	2	I37301	MHC class II histo
710	2	5.9	29	2	I37303	HLA-DR beta - huma
711	2	5.9	29	2	I37306	HLA-DR beta - huma
712	2	5.9	29	2	I50214	protein-tyrosine-p
713	2	5.9	29	2	S07771	histone H2B.2, spe
714	2	5.9	29	2	T04412	histone H3 - barle
715	2	5.9	29	2	S51070	ribosomal protein
716	2	5.9	29	2	S08555	ribosomal protein
717	2	5.9	29	2	PC4231	ribosomal protein
718	2	5.9	29	2	S10050	ribosomal protein
719	2	5.9	29	2	S10049	ribosomal protein
720	2	5.9	29	2	S26229	ribosomal protein
721	2	5.9	29	2	A27561	Meth A tumor-speci
722	2	5.9	29	2	S10725	calmodulin-binding
723	2	5.9	29	2	E33208	calreticulin, uter
724	2	5.9	29	2	C33208	calreticulin, slow
725	2	5.9	29	2	D33208	calreticulin, brai
726	2	5.9	29	2	A45474	thrombospondin 2 -
727	2	5.9	29	2	G39690	neural cell adhesi
728	2	5.9	29	2	A61166	endometrial proges
729	2	5.9	29	2	I52402	alpha-fetoprotein
730	2	5.9	29	2	S00564	enamel protein - r
731	2	5.9	29	2	S57232	homeotic protein s
732	2	5.9	29	2	S06854	chorion class B pr
733	2	5.9	29	2	A43038	auxin-binding prot
734	2	5.9	29	2	T12082	proline-rich prote
735	2	5.9	29	2	S70328	gamma35 secalin -
736	2	5.9	29	2	S29208	avenin gamma-3 - o
737	2	5.9	29	2	S07055	photosystem I prot
738	2	5.9	29	2	S05032	photosystem II pro
739	2	5.9	29	2	S08088	gene VII protein -
740	2	5.9	29	2	F42075	finger protein (cl
741	2	5.9	29	2	T51116	probable precorrin
742	2	5.9	29	2	A53145	high conductance c
743	2	5.9	29	2	A35121	hypothetical prote
744	2	5.9	29	2	S03277	photosystem II 5K
745	2	5.9	29	2	S63509	glycine reductase
746	2	5.9	29	2	A55891	delta-conotoxin Gm
747	2	5.9	29	2	S32730	homeotic protein -
748	2	5.9	29	2	S57225	labial protein (cl
749	2	5.9	29	2	S32732	homeotic protein -
750	2	5.9	29	2	S32734	homeotic protein -
751	2	5.9	29	2	S32733	homeotic protein -
752	2	5.9	29	2	S07513	gene 5.1 protein -
753	2	5.9	29	2	S14040	hypothetical prote
754	2	5.9	29	2	E64586	hypothetical prote

755	2	5.9	29	2	B64607	hypothetical prote
756	2	5.9	29	2	G83440	KdpF protein PA163
757	2	5.9	29	2	A49288	alcohol dehydrogen
758	2	5.9	29	2	B81136	hypothetical prote
759	2	5.9	29	2	A81078	hypothetical prote
760	2	5.9	29	2	B81006	hypothetical prote
761	2	5.9	29	2	S19943	aadB protein - Kle
762	2	5.9	29	2	A49914	S-layer protein va
763	2	5.9	29	2	B48363	2-hydroxyglutaryl-
764	2	5.9	29	2	C40638	orf 3' of cycI - R
765	2	5.9	29	2	S05224	photosystem I 4.8K
766	2	5.9	29	2	B56817	photosystem I chai
767	2	5.9	29	2	S74572	hypothetical prote
768	2	5.9	29	2	C60743	putrescine carbamo
769	2	5.9	29	2	S67989	HA-19/HA-52 protei
770	2	5.9	29	2	S14099	12-alpha-hydroxyst
771	2	5.9	29	2	S77569	plantaricin SA6 -
772	2	5.9	29	2	S21222	48K protein - Euba
773	2	5.9	29	2	S03947	hydrogen dehydroge
774	2	5.9	29	2	T34643	hypothetical prote
775	2	5.9	29	2	T37120	hypothetical prote
776	2	5.9	29	2	T36654	probable small mem
777	2	5.9	29	2	B43937	endo-1,4-beta-xyla
778	2	5.9	29	2	S09556	hypothetical prote
779	2	5.9	29	2	T06904	hypothetical prote
780	2	5.9	29	2	S73197	hypothetical prote
781	2	5.9	29	2	S78326	conserved hypothet
782	2	5.9	29	2	S78310	hypothetical prote
783	2	5.9	29	2	S78360	hypothetical prote
784	2	5.9	29	2	S01572	hypothetical prote
785	2	5.9	29	2	T07450	hypothetical prote
786	2	5.9	29	2	S01448	hypothetical prote
787	2	5.9	29	2	S38525	rRNA N-glycosidase
788	2	5.9	29	2	T52557	translation elonga
789	2	5.9	29	2	PQ0862	allantoinase (EC 3
790	2	5.9	29	2	PQ0486	globulin 2a - taro
791	2	5.9	29	2	S02200	prolamin alpha-1 -
792	2	5.9	29	2	A60683	malate dehydrogena
793	2	5.9	29	2	JQ0212	hypothetical 3K pr
794	2	5.9	29	2	S58541	hypothetical prote
795	2	5.9	29	2	PC2035	alanine transamina
796	2	5.9	29	2	S78714	protein YDR524w-a
797	2	5.9	29	2	S68094	2,3-dihydroxybenzo
798	2	5.9	29	2	B21112	variant surface gl
799	2	5.9	29	2	C60110	repetitive protein
800	2	5.9	29	2	A56591	E75 steroid recept
801	2	5.9	29	2	A61613	ceratotoxin A - Me
802	2	5.9	29	2	B61613	ceratotoxin B - Me
803	2	5.9	29	2	PH1230	lectin - namazu (f
804	2	5.9	29	2	A32860	biotin-binding pro
805	2	5.9	29	2	I50382	c-mil protein - ch
806	2	5.9	29	2	I50695	non-collagenous al
807	2	5.9	29	2	B54197	70k thyroid autoan
808	2	5.9	29	2	A35891	carcinoembryonic a
809	2	5.9	29	2	I77372	CD44SP - human
810	2	5.9	29	2	S54340	diazepam binding i
811	2	5.9	29	2	A41683	hyaluronate recept

812	2	5.9	29	2	C54037	splicing regulator
813	2	5.9	29	2	S35924	T-cell receptor ga
814	2	5.9	29	2	A60604	glutathione peroxi
815	2	5.9	29	2	A27688	mammary-derived gr
816	2	5.9	29	2	S57204	oviduct-specific s
817	2	5.9	29	2	I47025	antigen WC1 [impor
818	2	5.9	29	2	A49410	t-complex polypept
819	2	5.9	29	2	PS0125	H-2 class I histoc
820	2	5.9	29	2	S46929	tegl69 protein - m
821	2	5.9	29	2	S38749	vimentin homolog -
822	2	5.9	29	2	S42764	Ca2+/calmodulin-de
823	2	5.9	29	2	A49708	synaptosomal-assoc
824	2	5.9	29	2	H83777	hypothetical prote
825	2	5.9	29	2	C83833	hypothetical prote
826	2	5.9	29	2	F83870	hypothetical prote
827	2	5.9	29	2	B84144	hypothetical prote
828	2	5.9	29	2	PC4421	multactivase (EC 3
829	2	5.9	29	2	B85840	hypothetical prote
830	2	5.9	29	2	C85840	hypothetical prote
831	2	5.9	29	2	G86058	hypothetical prote
832	2	5.9	29	2	E89904	hypothetical prote
833	2	5.9	29	2	H89949	hypothetical prote
834	2	5.9	29	2	S17496	inorganic diphosph
835	2	5.9	29	2	PQ0782	NADH2 dehydrogenas
836	2	5.9	29	2	S34762	L-serine ammonia-l
837	2	5.9	29	2	AB0717	hypothetical prote
838	2	5.9	29	2	AC0717	hypothetical prote
839	2	5.9	29	2	AH2338	PetN protein [impo
840	2	5.9	29	4	I58970	hypothetical prote
841	2	5.9	30	1	AIBSAF	thermophilic amino
842	2	5.9	30	1	TIPU1W	trypsin inhibitor
843	2	5.9	30	1	OEON2K	beta-endorphin II
844	2	5.9	30	1	IRTRC3	protamine CIII, ma
845	2	5.9	30	1	IRTRC2	protamine Ia - rai
846	2	5.9	30	1	IRTR78	protamine CIII, mi
847	2	5.9	30	1	IRTR4	protamine pTP4 - r
848	2	5.9	30	1	CLHRY2	protamine YII - Pa
849	2	5.9	30	1	CLHR2A	protamine YII - At
850	2	5.9	30	1	SNUMP	sillucin - Rhizomu
851	2	5.9	30	2	I57689	ubiquinol-cytochro
852	2	5.9	30	2	I52254	gene CYP11B2 prote
853	2	5.9	30	2	B56859	fatty acid omega-h
854	2	5.9	30	2	A27375	photosystem I iron
855	2	5.9	30	2	S11131	NADH2 dehydrogenas
856	2	5.9	30	2	S14214	NADH2 dehydrogenas
857	2	5.9	30	2	S08202	peroxidase (EC 1.1
858	2	5.9	30	2	S08204	peroxidase (EC 1.1
859	2	5.9	30	2	S08203	peroxidase (EC 1.1
860	2	5.9	30	2	A39089	hydrogenase (EC 1.
861	2	5.9	30	2	I38066	nitric-oxide synth
862	2	5.9	30	2	I39799	CAT-66 - Bacillus
863	2	5.9	30	2	A18780	dimethylallyltrans
864	2	5.9	30	2	S03283	methionine adenosy
865	2	5.9	30	2	A28562	glutathione transf
866	2	5.9	30	2	B27103	aspartate transami
867	2	5.9	30	2	A27103	aspartate transami
868	2	5.9	30	2	I55427	aspartate transami

869	2	5.9	30	2	A49955	protein-tyrosine k
870	2	5.9	30	2	S68639	nigroxin A - black
871	2	5.9	30	2	S68640	nigroxin B - black
872	2	5.9	30	2	A05004	pancreatic ribonuc
873	2	5.9	30	2	A44598	endo-1,4-beta-xyla
874	2	5.9	30	2	PC2361	alpha-glucosidase
875	2	5.9	30	2	PX0073	epoxide hydrolase
876	2	5.9	30	2	B60291	30K serine protein
877	2	5.9	30	2	A27634	major fecal allerg
878	2	5.9	30	2	B27634	major fecal allerg
879	2	5.9	30	2	I77411	renin-2 - mouse (f
880	2	5.9	30	2	PC2328	proteasome endopep
881	2	5.9	30	2	A34486	inorganic diphosph
882	2	5.9	30	2	S21816	H+-exporting ATPas
883	2	5.9	30	2	S21814	H+-exporting ATPas
884	2	5.9	30	2	S74121	fructose-bisphosph
885	2	5.9	30	2	S25666	phosphopyruvate hy
886	2	5.9	30	2	S69600	peptidylprolyl iso
887	2	5.9	30	2	A60517	alpha-1-antitrypsi
888	2	5.9	30	2	S24979	proteinase inhibit
889	2	5.9	30	2	JX0057	trypsin inhibitor
890	2	5.9	30	2	JS0579	squash-type trypsi
891	2	5.9	30	2	JQ1958	trypsin inhibitor
892	2	5.9	30	2	PC1113	proteinase inhibit
893	2	5.9	30	2	C42842	antifungal 2S stor
894	2	5.9	30	2	S70341	napin large chain
895	2	5.9	30	2	S70343	napin large chain
896	2	5.9	30	2	A33308	thrombomodulin - r
897	2	5.9	30	2	S01657	atrial natriuretic
898	2	5.9	30	2	A61130	somatotropin - Ame
899	2	5.9	30	2	S44473	glucagon-like pept
900	2	5.9	30	2	A59076	defensin alpha-1 -
901	2	5.9	30	2	B59076	defensin alpha-2 -
902	2	5.9	30	2	C59076	defensin alpha-3 -
903	2	5.9	30	2	B60791	toxin II.6 - scorp
904	2	5.9	30	2	A31187	neurotoxin II.22.5
905	2	5.9	30	2	I68109	interferon alpha-W
906	2	5.9	30	2	C49533	T-cell receptor al
907	2	5.9	30	2	S20778	Ig heavy chain V r
908	2	5.9	30	2	PL0092	Ig heavy chain V r
909	2	5.9	30	2	PH0245	T-cell receptor Vb
910	2	5.9	30	2	PH0228	T-cell receptor Vb
911	2	5.9	30	2	PH0252	T-cell receptor Vb
912	2	5.9	30	2	PH0882	Ig kappa chain V r
913	2	5.9	30	2	E31461	T-cell receptor de
914	2	5.9	30	2	PH0235	T-cell receptor Vb
915	2	5.9	30	2	A49533	T-cell receptor al
916	2	5.9	30	2	C27579	T-cell receptor be
917	2	5.9	30	2	I37626	Fc gamma (IgG) rec
918	2	5.9	30	2	PS0121	H-2 class I histoc
919	2	5.9	30	2	S74192	crotoxin inhibitor
920	2	5.9	30	2	A05253	hemoglobin epsilon
921	2	5.9	30	2	A21680	hemoglobin epsilon
922	2	5.9	30	2	A05254	hemoglobin epsilon
923	2	5.9	30	2	S68618	histone H2B - sea
924	2	5.9	30	2	PD0014	cAMP response elem
925	2	5.9	30	2	PN0651	restriction endonu

926	2	5.9	30	2	S11613	ribosomal protein
927	2	5.9	30	2	A60511	gamma-crystallin -
928	2	5.9	30	2	I49412	gamma-crystallin-3
929	2	5.9	30	2	S12965	gamma-crystallin -
930	2	5.9	30	2	S69269	ezrin homolog - bo
931	2	5.9	30	2	A61189	tubulin beta chain
932	2	5.9	30	2	I52806	Duchenne muscular
933	2	5.9	30	2	S21153	calcium-binding pr
934	2	5.9	30	2	A26188	lipocortin I - pig
935	2	5.9	30	2	A56790	annexin, isoform P
936	2	5.9	30	2	A34622	fibrinogen beta ch
937	2	5.9	30	2	A03148	retinol-binding pr
938	2	5.9	30	2	A48299	taurine transporte
939	2	5.9	30	2	B61511	serum albumin, mil
940	2	5.9	30	2	B39819	neutrophil chemota
941	2	5.9	30	2	A38933	vitronectin - bovi
942	2	5.9	30	2	S57234	fushi tarazu segme
943	2	5.9	30	2	S69124	rRNA N-glycosidase
944	2	5.9	30	2	S69125	rRNA N-glycosidase
945	2	5.9	30	2	S07065	rRNA N-glycosidase
946	2	5.9	30	2	A31836	17K antigen - Rick
947	2	5.9	30	2	S14062	hypothetical prote
948	2	5.9	30	2	PQ0669	photosystem I 17.5
949	2	5.9	30	2	E45095	photosystem I ligh
950	2	5.9	30	2	B45095	photosystem I ligh
951	2	5.9	30	2	A44913	34K core flagella
952	2	5.9	30	2	B24987	regulatory protein
953	2	5.9	30	2	S30757	genome polyprotein
954	2	5.9	30	2	S30760	genome polyprotein
955	2	5.9	30	2	S30759	genome polyprotein
956	2	5.9	30	2	B44314	intracisternal A p
957	2	5.9	30	2	S13753	replication initia
958	2	5.9	30	2	S26175	tail tubular prote
959	2	5.9	30	2	S69352	N-methylhydantoin
960	2	5.9	30	2	S68312	glucuronosyltransf
961	2	5.9	30	2	PH1228	D-aminoacylase (EC
962	2	5.9	30	2	S42364	aromatic-amino-aci
963	2	5.9	30	2	S05223	photosystem I 6.5K
964	2	5.9	30	2	S28991	antifungal protein
965	2	5.9	30	2	PC2307	X-Pro aminopeptida
966	2	5.9	30	2	PQ0484	globulin lb - taro
967	2	5.9	30	2	C43591	51K outer membrane
968	2	5.9	30	2	B43591	45K outer membrane
969	2	5.9	30	2	S06411	killer plasmid 28K
970	2	5.9	30	2	B49292	GDP dissociation i
971	2	5.9	30	2	A60914	pheromone-binding
972	2	5.9	30	2	PS0437	potassium channel
973	2	5.9	30	2	PS0438	potassium channel
974	2	5.9	30	2	A47607	immunogenic protei
975	2	5.9	30	2	S02088	blood group Rh-rel
976	2	5.9	30	2	S29138	aniline monooxygen
977	2	5.9	30	2	S57227	proboscipedia prot
978	2	5.9	30	2	H95008	hypothetical prote
979	2	5.9	30	2	C95030	hypothetical prote
980	2	5.9	30	2	G95031	hypothetical prote
981	2	5.9	30	2	E95079	hypothetical prote
982	2	5.9	30	2	F95118	hypothetical prote

983	2	5.9	30	2	E95145	hypothetical prote
984	2	5.9	30	2	F89406	protein R10E8.7 [i
985	2	5.9	30	2	E84786	hypothetical prote
986	2	5.9	30	2	A84412	hypothetical prote
987	2	5.9	30	2	C84481	hypothetical prote
988	2	5.9	30	2	B47483	cysteine-rich para
989	2	5.9	30	2	S15141	hypothetical prote
990	2	5.9	30	2	S13985	hypothetical prote
991	2	5.9	30	2	S14038	hypothetical prote
992	2	5.9	30	2	S13994	hypothetical prote
993	2	5.9	30	2	A72205	hypothetical prote
994	2	5.9	30	2	E72356	hypothetical prote
995	2	5.9	30	2	H72312	hypothetical prote
996	2	5.9	30	2	S66448	trimethylamine deh
997	2	5.9	30	2	A70105	conserved hypothet
998	2	5.9	30	2	F70118	hypothetical prote
999	2	5.9	30	2	D70144	hypothetical prote
1000	2	5.9	30	2	H70152	hypothetical prote

ALIGNMENTS

RESULT 1

A84241

hypothetical protein Vng0840h [imported] - Halobacterium sp. NRC-1

C;Species: Halobacterium sp. NRC-1

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C;Accession: A84241

R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.;
Lasky, S.R.; Baliga, N.; Thorsson, V.; Sbrogna, J.; Swartzell, S.; Weir, D.;
Hall, J.; Dahl, T.A.; Welti, R.; Goo, Y.A.; Leithauser, B.; Keller, K.; Cruz,
R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablonski, P.E.; Krebs, M.P.;
Angevine, C.M.; Dale, H.; Isenbarger, T.A.; Peck, R.F.; Pohlschrod, M.; Spudich,
J.L.; Jung, K.H.; Alam, M.; Freitas, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe,
T.M.; Liang, P.; Riley, M.; Hood, L.; DasSarma, S.

A;Title: Genome sequence of Halobacterium species NRC-1.

A;Reference number: A84160; MUID:20504483; PMID:11016950

A;Accession: A84241

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-34 <STO>

A;Cross-references: GB:AE004437; NID:g10580410; PIDN:AAG19293.1; GSPDB:GN00138

C;Genetics:

A;Gene: VNG0840H

Query Match 14.7%; Score 5; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	24	LRKKL	28
Db	26	LRKKL	30

RESULT 2

B97032

transcription regulator, AcrR family [imported] - Clostridium acetobutylicum

C;Species: Clostridium acetobutylicum

C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001

C;Accession: B97032

R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, H.M.; Dubois, J.; Qiu, D.; Hitti, J.; Wolf, Y.I.; Tatusov, R.L.; Sabathe, F.; Doucette-Stamm, L.; Soucaille, P.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

J. Bacteriol. 183, 4823-4838, 2001

A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clostridium acetobutylicum.

A;Reference number: A96900; MUID:21359325; PMID:21359325

A;Accession: B97032

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-34 <KUR>

A;Cross-references: GB:AE001437; PIDN:AAK79045.1; PID:g15023984; GSPDB:GN00168

A;Experimental source: Clostridium acetobutylicum ATCC824

C;Genetics:

A;Gene: CAC1071

Query Match 14.7%; Score 5; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEI 5
|||||
Db 30 SVSEI 34

RESULT 3

E95098

hypothetical protein SP0853 [imported] - Streptococcus pneumoniae (strain TIGR4)

C;Species: Streptococcus pneumoniae

C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001

C;Accession: E95098

R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heidelberg, J.; DeBoy, R.T.; Haft, D.H.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.; Kolonay, J.F.; Nelson, W.C.; Peterson, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, E.; Khouri, H.; Wolf, A.M.; Utterback, T.R.; Hansen, C.L.; McDonald, L.A.; Feldblyum, T.V.; Angiuoli, S.; Dickinson, T.; Hickey, E.K.; Holt, I.E.

Science 293, 498-506, 2001

A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, D.A.; Hollingshead, S.K.; Fraser, C.M.

A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.

A;Reference number: A95000; MUID:21357209; PMID:11463916

A;Accession: E95098

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-35 <KUR>

A;Cross-references: GB:AE005672; PIDN:AAK74982.1; PID:g14972326; GSPDB:GN00164; TIGR:SP4SP0853

A;Experimental source: strain TIGR4

C;Genetics:
A;Gene: SP0853

Query Match 14.7%; Score 5; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQD 30
|||||
Db 30 KKLQD 34

RESULT 4

T09594
gene LFY protein - Monterey pine (fragment)
C;Species: Pinus radiata (Monterey pine)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C;Accession: T09594
R;Izquierdo, L.Y.; Vergara, R.F.; Alvarez-Buylla, E.R.
submitted to the EMBL Data Library, August 1996
A;Description: Partial characterization of Pinus radiata meristem identity
homolog gene (LFY).
A;Reference number: Z16756
A;Accession: T09594
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-28 <IZQ>
A;Cross-references: EMBL:U66725; NID:g1513305; PID:g1513306
C;Genetics:
A;Gene: LFY
C;Function:
A;Description: controls meristem identity

Query Match 11.8%; Score 4; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKK 27
|||||
Db 15 LRKK 18

RESULT 5

A55527
pyrroloquinoline quinone precursor pqqD - Methylobacterium extorquens
C;Species: Methylobacterium extorquens
C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 18-Feb-2000
C;Accession: A55527
R;Morris, C.J.; Biville, F.; Turlin, E.; Lee, E.; Ellermann, K.; Fan, W.H.;
Ramamoorthi, R.; Springer, A.L.; Lidstrom, M.E.
J. Bacteriol. 176, 1746-1755, 1994
A;Title: Isolation, phenotypic characterization, and complementation analysis of
mutants of Methylobacterium extorquens AM1 unable to synthesize pyrroloquinoline
quinone and sequences of pqqD, pqqG, and pqqC.
A;Reference number: A55527; MUID:94179111; PMID:8132470
A;Accession: A55527
A;Status: preliminary

A;Molecule type: DNA
A;Residues: 1-29 <MOR>
A;Cross-references: GB:L25889; NID:g414589; PIDN:AAA17878.1; PID:g414590
C;Genetics:
A;Gene: pqqD
C;Superfamily: pyrroloquinoline quinone precursor pqqA
C;Keywords: quinoprotein
F;16,20/Product: pyrroloquinoline quinone #status predicted <MAT>
F;16-20/Cross-link: pyrroloquinoline quinone (Glu, Tyr) #status predicted

Query Match 11.8%; Score 4; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSEI 5
|||
Db 8 VSEI 11

RESULT 6

S01614
dystrophin - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
C;Accession: S01614
R;Nudel, U.; Robzyk, K.; Yaffe, D.
Nature 331, 635-638, 1988
A;Title: Expression of the putative Duchenne muscular dystrophy gene in
differentiated myogenic cell cultures and in the brain.
A;Reference number: S01614; MUID:88122671; PMID:3340214
A;Accession: S01614
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-29 <NUD>
A;Cross-references: EMBL:X07000; NID:g56137; PIDN:CAA30057.1; PID:g1334214
C;Genetics:
A;Map position: X
C;Superfamily: dystrophin; alpha-actinin actin-binding domain homology;
spectrin/dystrophin repeat homology; WW repeat homology
C;Keywords: actin binding; cytoskeleton

Query Match 11.8%; Score 4; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 KLQD 30
|||
Db 12 KLQD 15

RESULT 7

I78537
copper transporting P-type ATPase - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C;Accession: I78537
R;Thomas, G.R.; Forbes, J.R.; Roberts, E.A.; Walshe, J.M.; Cox, D.W.

Nature Genet. 9, 210-217, 1995

A;Title: The Wilson disease gene: spectrum of mutations and their consequences.

A;Reference number: I58128; MUID:95235569; PMID:7626145

A;Accession: I78537

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-29 <RES>

A;Cross-references: GB:S77450; NID:g957354; PIDN:AAB34087.1; PID:g957355

C;Genetics:

A;Gene: GDB:ATP7B

A;Cross-references: GDB:120494; OMIM:277900

A;Map position: 13q14.3-13q21.1

Query Match 11.8%; Score 4; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SEIQ 6
 ||||
Db 14 SEIQ 17

RESULT 8

S78412

ribosomal protein RL22/RL24, mitochondrial [validated] - rat (tentative sequence) (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 25-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jul-2000

C;Accession: S78412; S78413

R;Goldschmidt-Reisin, S.; Graack, H.R.

submitted to the Protein Sequence Database, February 1998

A;Reference number: S78411

A;Accession: S78412

A;Molecule type: protein

A;Residues: 1-29 <GOL>

A;Note: the protein is designated as mitochondrial ribosomal protein L22

A;Accession: S78413

A;Molecule type: protein

A;Residues: 1-10,'XXP',14-15,'X',17-24 <GO2>

A;Note: the protein is designated as mitochondrial ribosomal protein L24

C;Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 11.8%; Score 4; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKK 27
 ||||
Db 4 LRKK 7

RESULT 9

S63531

hypothetical protein 1 - Sulfolobus solfataricus (fragment)

C;Species: Sulfolobus solfataricus

C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999

C;Accession: S63531

R;Jones, C.E.; Fleming, T.M.; Cowan, D.A.; Littlechild, J.A.; Piper, P.W.
Eur. J. Biochem. 233, 800-808, 1995
A;Title: The phosphoglycerate kinase and glyceraldehyde-3-phosphate
dehydrogenase genes from the thermophilic archaeon Sulfolobus solfataricus
overlap by 8-bp: isolation, sequencing of the genes and expression in
Escherichia coli.
A;Reference number: S63528; MUID:96085144; PMID:8521845
A;Accession: S63531
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-30 <JON>
A;Cross-references: EMBL:X80178

Query Match 11.8%; Score 4; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 WLRK 26
|||
Db 11 WLRK 14

RESULT 10

S44471
glucagon G1 - North American paddlefish (Polyodon spathula)
C;Species: Polyodon spathula
C;Date: 18-Sep-1997 #sequence_revision 18-Sep-1997 #text_change 07-May-1999
C;Accession: S44471
R;Nguyen, T.M.; Mommsen, T.P.; Mims, S.M.; Conlon, J.M.
Biochem. J. 300, 339-345, 1994
A;Title: Characterization of insulins and proglucagon-derived peptides from a
phylogenetically ancient fish, the paddlefish (Polyodon spathula).
A;Reference number: S44467; MUID:94271144; PMID:8002937
A;Accession: S44471
A;Molecule type: protein
A;Residues: 1-31 <NGU>
A;Experimental source: pancreas
C;Superfamily: glucagon
C;Keywords: carbohydrate metabolism; duplication; hormone; pancreas
F;1-31/Product: glucagon G1 #status predicted <MAT>

Query Match 11.8%; Score 4; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 VEWL 24
|||
Db 23 VEWL 26

RESULT 11

S44472
glucagon G2 - North American paddlefish (Polyodon spathula)
C;Species: Polyodon spathula
C;Date: 19-Mar-1997 #sequence_revision 12-Dec-1997 #text_change 07-May-1999
C;Accession: S44472
R;Nguyen, T.M.; Mommsen, T.P.; Mims, S.M.; Conlon, J.M.

Biochem. J. 300, 339-345, 1994

A;Title: Characterization of insulins and proglucagon-derived peptides from a phylogenetically ancient fish, the paddlefish (*Polyodon spathula*).

A;Reference number: S44467; MUID:94271144; PMID:8002937

A;Accession: S44472

A;Molecule type: protein

A;Residues: 1-31 <NGU>

A;Note: the sequence from Fig. 3 is inconsistent with that from Fig. 5 in having 29-Glu

C;Superfamily: glucagon

C;Keywords: carbohydrate metabolism; duplication; hormone; pancreas

F;1-31/Product: glucagon G2 #status predicted <GCN>

Query Match 11.8%; Score 4; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 VEWL 24
||||
Db 23 VEWL 26

RESULT 12

D70236

hypothetical protein BBH11 - Lyme disease spirochete plasmid H/lp28-3

C;Species: *Borrelia burgdorferi* (Lyme disease spirochete)

C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 08-Oct-1999

C;Accession: D70236

R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White, O.; Ketchum, K.A.; Dodson, R.; Hickey, E.K.; Gwinn, M.; Dougherty, B.; Tomb, J.F.; Fleischmann, R.D.; Richardson, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, R.V.; Palmer, N.; Adams, M.D.; Gocayne, J.; Weidman, J.; Utterback, T.; Watthey, L.; McDonald, L.; Artiach, P.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.

Nature 390, 580-586, 1997

A;Authors: Smith, H.O.; Venter, J.C.

A;Title: Genomic sequence of a Lyme disease spirochaete, *Borrelia burgdorferi*.

A;Reference number: A70100; MUID:98065943; PMID:9403685

A;Accession: D70236

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-31 <KLE>

A;Cross-references: GB:AE000784; NID:g2690041; PIDN:AAC66002.1; PID:g2690058;

TIGR:BBH11

A;Experimental source: strain B31

C;Genetics:

A;Genome: plasmid

Query Match 11.8%; Score 4; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29
||||
Db 26 KKLQ 29

RESULT 13

F23454

ovalbumin phosphoserine peptide - fulvous whistling-duck (fragments)

C;Species: Dendrocygna bicolor (fulvous whistling-duck)

C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 13-Mar-1998

C;Accession: F23454

R;Henderson, J.Y.; Moir, A.J.G.; Fothergill, L.A.; Fothergill, J.E.

Eur. J. Biochem. 114, 439-450, 1981

A;Title: Sequences of sixteen phosphoserine peptides from ovalbumins of eight species.

A;Reference number: A91106; MUID:81164535; PMID:6783411

A;Accession: F23454

A;Molecule type: protein

A;Residues: 1-32 <HEN>

C;Superfamily: antithrombin III

Query Match 11.8%; Score 4; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSE 4
|||
Db 26 SVSE 29

RESULT 14

D31461

T-cell receptor delta chain BDN7, thymus - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 05-Oct-1989 #sequence_revision 05-Oct-1989 #text_change 30-May-1997

C;Accession: D31461

R;Lacy, M.J.; McNeil, L.K.; Roth, M.E.; Kranz, D.M.

Proc. Natl. Acad. Sci. U.S.A. 86, 1023-1026, 1989

A;Title: T-cell receptor delta-chain diversity in peripheral lymphocytes.

A;Reference number: A31461; MUID:89128840; PMID:2783779

A;Accession: D31461

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-32 <LAC>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: T-cell receptor

Query Match 11.8%; Score 4; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 MERV 21
|||
Db 8 MERV 11

RESULT 15

G84161

hypothetical protein Vng0019h [imported] - Halobacterium sp. NRC-1

C;Species: Halobacterium sp. NRC-1

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C;Accession: G84161
 R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.;
 Lasky, S.R.; Baliga, N.; Thorsson, V.; Sbrogna, J.; Swartzell, S.; Weir, D.;
 Hall, J.; Dahl, T.A.; Welte, R.; Goo, Y.A.; Leithauser, B.; Keller, K.; Cruz,
 R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablonski, P.E.; Krebs, M.P.;
 Angevine, C.M.; Dale, H.; Isenbarger, T.A.; Peck, R.F.; Pohlschrod, M.; Spudich,
 J.L.; Jung, K.H.; Alam, M.; Freitas, T.
 Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
 A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe,
 T.M.; Liang, P.; Riley, M.; Hood, L.; DasSarma, S.
 A;Title: Genome sequence of Halobacterium species NRC-1.
 A;Reference number: A84160; MUID:20504483; PMID:11016950
 A;Accession: G84161
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-32 <STO>
 A;Cross-references: GB:AE004437; NID:g10579667; PIDN:AAG18659.1; GSPDB:GN00138
 C;Genetics:
 A;Gene: VNG0019H

Query Match 11.8%; Score 4; DB 2; Length 32;
 Best Local Similarity 100.0%; Pred. No. 1e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 KLQD 30
 ||||
 Db 13 KLQD 16

RESULT 16

E81714
 hypothetical protein TC0337 [imported] - Chlamydia muridarum (strain Nigg)
 C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
 C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000
 C;Accession: E81714
 R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.;
 Hickey, E.K.; Peterson, J.; Utterback, T.; Berry, K.; Bass, S.; Linher, K.;
 Weidman, J.; Khouri, H.; Craven, B.; Bowman, C.; Dodson, R.; Gwinn, M.; Nelson,
 W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, S.L.; Eisen, J.; Fraser,
 C.M.
 Nucleic Acids Res. 28, 1397-1406, 2000
 A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae
 AR39.
 A;Reference number: A81500; MUID:20150255; PMID:10684935
 A;Accession: E81714
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-33 <TET>
 A;Cross-references: GB:AE002301; GB:AE002160; NID:g7190372; PIDN:AAF39200.1;
 PID:g7190379; GSPDB:GN00121; TIGR:TC0337
 A;Experimental source: strain Nigg (MoPn)
 C;Genetics:
 A;Gene: TC0337

Query Match 11.8%; Score 4; DB 2; Length 33;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKK 27
|||
Db 26 LRKK 29

RESULT 17

D23454

ovalbumin phosphoserine peptide - golden pheasant (fragments)

C;Species: Chrysolophus pictus (golden pheasant)

C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 13-Mar-1998

C;Accession: D23454

R;Henderson, J.Y.; Moir, A.J.G.; Fothergill, L.A.; Fothergill, J.E.

Eur. J. Biochem. 114, 439-450, 1981

A;Title: Sequences of sixteen phosphoserine peptides from ovalbumins of eight species.

A;Reference number: A91106; MUID:81164535; PMID:6783411

A;Accession: D23454

A;Molecule type: protein

A;Residues: 1-35 <HEN>

C;Superfamily: antithrombin III

Query Match 11.8%; Score 4; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSE 4
|||
Db 29 SVSE 32

RESULT 18

G23454

ovalbumin phosphoserine peptide - magpie goose (fragments)

C;Species: Anseranas semipalmata (magpie goose)

C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 13-Mar-1998

C;Accession: G23454

R;Henderson, J.Y.; Moir, A.J.G.; Fothergill, L.A.; Fothergill, J.E.

Eur. J. Biochem. 114, 439-450, 1981

A;Title: Sequences of sixteen phosphoserine peptides from ovalbumins of eight species.

A;Reference number: A91106; MUID:81164535; PMID:6783411

A;Accession: G23454

A;Molecule type: protein

A;Residues: 1-35 <HEN>

C;Superfamily: antithrombin III

Query Match 11.8%; Score 4; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSE 4
|||
Db 29 SVSE 32

RESULT 19

D82125

hypothetical protein VC2034 [imported] - *Vibrio cholerae* (strain N16961 serogroup O1)

C;Species: *Vibrio cholerae*

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001

C;Accession: D82125

R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, E.K.; Peterson, J.D.; Umayam, L.A.; Gill, S.R.; Nelson, K.E.; Read, T.D.; Tettelin, H.; Richardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.; McDonald, L.; Utterback, T.; Fleishmann, R.D.; Nierman, W.C.; White, O.; Salzberg, S.L.; Smith, H.O.; Colwell, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000

A;Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.

A;Reference number: A82035; MUID:20406833; PMID:10952301

A;Accession: D82125

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-35 <HEI>

A;Cross-references: GB:AE004278; GB:AE003852; NID:g9656579; PIDN:AAF95182.1; GSPDB:GN00126; TIGR:VC2034

A;Experimental source: serogroup O1; strain N16961; biotype El Tor

C;Genetics:

A;Gene: VC2034

A;Map position: 1

Query Match 11.8%; Score 4; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29
|||
Db 24 KKLQ 27

RESULT 20

S70806

hypothetical protein 5 - *Vibrio cholerae* (fragment)

N;Alternate names: flagellar protein flaA homolog

C;Species: *Vibrio cholerae*

C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 26-Aug-1999

C;Accession: S70806

R;Camilli, A.; Mekalanos, J.J.

Mol. Microbiol. 18, 671-683, 1995

A;Title: Use of recombinase gene fusions to identify *Vibrio cholerae* genes induced during infection.

A;Reference number: S70798; MUID:96414469; PMID:8817490

A;Accession: S70806

A;Status: preliminary; nucleic acid sequence not shown

A;Molecule type: DNA

A;Residues: 1-36 <CAM>

A;Cross-references: EMBL:U25820; NID:g1165195; PIDN:AAC43560.1; PID:g1165196

C;Superfamily: flagellin

Query Match 11.8%; Score 4; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 SMER 20
||||
Db 14 SMER 17

RESULT 21

F95057

hypothetical protein SP0497 [imported] - Streptococcus pneumoniae (strain TIGR4)

C;Species: Streptococcus pneumoniae

C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001

C;Accession: F95057

R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heidelberg, J.; DeBoy, R.T.; Haft, D.H.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.; Kolonay, J.F.; Nelson, W.C.; Peterson, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, E.; Khouri, H.; Wolf, A.M.; Utterback, T.R.; Hansen, C.L.; McDonald, L.A.; Feldblyum, T.V.; Angiuoli, S.; Dickinson, T.; Hickey, E.K.; Holt, I.E.

Science 293, 498-506, 2001

A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.;

Morrison, D.A.; Hollingshead, S.K.; Fraser, C.M.

A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.

A;Reference number: A95000; MUID:21357209; PMID:11463916

A;Accession: F95057

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-36 <KUR>

A;Cross-references: GB:AE005672; PIDN:AAK74655.1; PID:g14971969; GSPDB:GN00164; TIGR:SP4SP0497

A;Experimental source: strain TIGR4

C;Genetics:

A;Gene: SP0497

Query Match 11.8%; Score 4; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29
||||
Db 10 KKLQ 13

RESULT 22

A84774

hypothetical protein At2g35870 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C;Accession: A84774

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; Mason, T.M.; Bowman, C.L.; Barnstead, M.E.; Feldblyum, T.V.; Buell, C.R.; Ketchum, K.A.; Lee, J.J.; Ronning, C.M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.J.; Gill, J.E.; Adams, M.D.; Carrera, A.J.; Creasy, T.H.; Goodman, H.M.; Somerville, C.R.; Copenhaver, G.P.; Preuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.C.

Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: A84774

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-36 <STO>

A;Cross-references: GB:AE002093; NID:g4510382; PIDN:AAD21470.1; GSPDB:GN00139

C;Genetics:

A;Gene: At2g35870

A;Map position: 2

Query Match 11.8%; Score 4; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29

||||

Db 4 KKLQ 7

RESULT 23

S46227

hypothetical protein - *Streptomyces chrysomallus* (fragment)

C;Species: *Streptomyces chrysomallus*

C;Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 28-May-1999

C;Accession: S46227

R;Pahl, A.; Keller, U.

EMBO J. 13, 3472-3480, 1994

A;Title: *Streptomyces chrysomallus* FKBP-33 is a novel immunophilin consisting of two FK506 binding domains; its gene is transcriptionally coupled to the FKBP-12 gene.

A;Reference number: S46227; MUID:94341259; PMID:8062824

A;Accession: S46227

A;Molecule type: DNA

A;Residues: 1-36 <PAH>

A;Cross-references: GB:Z34523; NID:g535270; PIDN:CAA84281.1; PID:g633645

A;Experimental source: strain ATCC 11523

Query Match 11.8%; Score 4; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 ERVE 22

||||

Db 27 ERVE 30

RESULT 24

B60963

charybdotoxin 2 - scorpion (*Leiurus quinquestriatus*)

C;Species: *Leiurus quinquestriatus hebraeus*

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999

C;Accession: B60963

R;Lucchesi, K.; Ravindran, A.; Young, H.; Moczydlowski, E.

J. Membr. Biol. 109, 269-281, 1989

A;Title: Analysis of the blocking activity of charybdotoxin homologs and iodinated derivatives against Ca(2+)-activated K⁺ channels.
A;Reference number: A60963; MUID:90012179; PMID:2477548
A;Accession: B60963
A;Molecule type: protein
A;Residues: 1-37 <LUC>
C;Superfamily: kaliotoxin
C;Keywords: neurotoxin; potassium channel inhibitor; pyroglutamic acid; venom
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;7-28,13-33,17-35/Disulfide bonds: #status predicted

Query Match 11.8%; Score 4; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NRGK 13
 ||||
Db 24 NRGK 27

RESULT 25

S71912

hemoglobin, extracellular, chain A1 - polychaete (*Perinereis aibuhitensis*) (fragment)

C;Species: *Perinereis aibuhitensis*

C;Date: 14-Apr-1998 #sequence_revision 08-May-1998 #text_change 02-Jul-1998

C;Accession: S71912

R;Matsubara, K.; Yamaki, M.; Nagayama, K.; Imai, K.; Ishii, H.; Gotoh, T.; Ebina, S.

Biochim. Biophys. Acta 1290, 215-223, 1996

A;Title: Wheat germ agglutinin-reactive chains of giant hemoglobin from the polychaete *Perinereis aibuhitensis*.

A;Reference number: S71912; MUID:96350431; PMID:8765123

A;Accession: S71912

A;Molecule type: protein

A;Residues: 1-37 <MAT>

C;Superfamily: globin; globin homology

C;Keywords: chromoprotein; heme; iron; oxygen carrier

Query Match 11.8%; Score 4; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 ERVE 22
 ||||
Db 25 ERVE 28

RESULT 26

T12635

homeotic protein HAHB-2 - common sunflower (fragment)

C;Species: *Helianthus annuus* (common sunflower)

C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 21-Jul-2000

C;Accession: T12635

R;Chan, R.L.; Gonzalez, D.H.

Plant Physiol. 106, 1687-1688, 1994

A;Title: A cDNA encoding an HD-zip protein from sunflower.

A;Reference number: Z17563; MUID:95148747; PMID:7846169
A;Accession: T12635
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-37 <CHA>
A;Cross-references: EMBL:L22849; NID:g349258; PIDN:AAA63766.1; PID:g349259
C;Keywords: DNA binding; homeobox; transcription regulation

Query Match 11.8%; Score 4; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 25 RKKL 28
 ||||
Db 6 RKKL 9

RESULT 27

CKFHCS

sarcotoxin IC - flesh fly (*Sarcophaga peregrina*)

C;Species: *Sarcophaga peregrina*

C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 08-Dec-1995

C;Accession: C22625

R;Okada, M.; Natori, S.

J. Biol. Chem. 260, 7174-7177, 1985

A;Title: Primary structure of sarcotoxin I, an antibacterial protein induced in the hemolymph of *Sarcophaga peregrina* (flesh fly) larvae.

A;Reference number: A92536; MUID:85207747; PMID:3888997

A;Accession: C22625

A;Molecule type: protein

A;Residues: 1-39 <OKA>

C;Comment: Sarcotoxins, which are potent bactericidal proteins, are produced in response to injury. They are cytotoxic to both Gram positive and Gram negative bacteria.

C;Superfamily: cecropin

C;Keywords: amidated carboxyl end; antibacterial; hemolymph

F;39/Modified site: amidated carboxyl end (Arg) #status predicted

Query Match 11.8%; Score 4; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 WLRK 26
 ||||
Db 2 WLRK 5

RESULT 28

S71913

hemoglobin, extracellular, chain A2 - polychaete (*Perinereis aibuhitensis*) (fragment)

C;Species: *Perinereis aibuhitensis*

C;Date: 14-Apr-1998 #sequence_revision 08-May-1998 #text_change 02-Jul-1998

C;Accession: S71913

R;Matsubara, K.; Yamaki, M.; Nagayama, K.; Imai, K.; Ishii, H.; Gotoh, T.; Ebina, S.

Biochim. Biophys. Acta 1290, 215-223, 1996

A;Title: Wheat germ agglutinin-reactive chains of giant hemoglobin from the polychaete *Perinereis aibuhitensis*.

A;Reference number: S71912; MUID:96350431; PMID:8765123

A;Accession: S71913

A;Molecule type: protein

A;Residues: 1-39 <MAT>

C;Superfamily: globin; globin homology

C;Keywords: chromoprotein; heme; iron; oxygen carrier

Query Match 11.8%; Score 4; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 ERVE 22
 ||||
Db 27 ERVE 30

RESULT 29

S77164

ycf32 protein - *Synechocystis* sp. (strain PCC 6803)

N;Alternate names: protein sml0007

C;Species: *Synechocystis* sp.

A;Variety: PCC 6803

C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000

C;Accession: S77164

R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; Hirose, M.; Sugiura, M.; Sasamoto, S.; Kimura, T.; Hosouchi, T.; Matsuno, A.; Muraki, A.; Nakazaki, N.; Naruo, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, M.; Tabata, S.

DNA Res. 3, 109-136, 1996

A;Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis* sp. PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.

A;Reference number: S74322; MUID:97061201; PMID:8905231

A;Accession: S77164

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-39 <KAN>

A;Cross-references: EMBL:D90908; GB:AB001339; NID:g1652725; PIDN:BAA17722.1; PID:g1652803

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C;Genetics:

A;Gene: ycf32

C;Superfamily: hypothetical protein ycf32

Query Match 11.8%; Score 4; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 LQDV 31
 ||||
Db 31 LQDV 34

RESULT 30

A42272

brain-type creatine kinase, peptide B - spiny dogfish (fragment)

C;Species: Squalus acanthias (spiny dogfish)

C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 11-Apr-1997

C;Accession: A42272

R;Friedman, D.L.; Roberts, R.

J. Biol. Chem. 267, 4270-4276, 1992

A;Title: Purification and localization of brain-type creatine kinase in sodium chloride transporting epithelia of the spiny dogfish, Squalus acanthias.

A;Reference number: A42272; MUID:92156175; PMID:1310991

A;Accession: A42272

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-28 <FRI>

A;Note: sequence extracted from NCBI backbone (NCBIP:82919)

C;Superfamily: creatine kinase; creatine kinase repeat homology

Query Match 8.8%; Score 3; DB 2; Length 28;

Best Local Similarity 100.0%; Pred. No. 1.1e+04;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKL 28

|||

Db 10 KKL 12

RESULT 31

C32416

phospholipase A2 (EC 3.1.1.4) pseudexin chain C - red-bellied black snake (fragment)

C;Species: Pseudechis porphyriacus (red-bellied black snake)

C;Date: 05-Oct-1989 #sequence_revision 05-Oct-1989 #text_change 23-Jun-1993

C;Accession: C32416

R;Schmidt, J.J.; Middlebrook, J.L.

Toxicon 27, 805-818, 1989

A;Title: Purification, sequencing and characterization of pseudexin phospholipases A-2 from Pseudechis porphyriacus (Australian red-bellied black snake).

A;Reference number: A32416; MUID:89388835; PMID:2675391

A;Accession: C32416

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-28 <SCH>

C;Superfamily: phospholipase A2

C;Keywords: carboxylic ester hydrolase

Query Match 8.8%; Score 3; DB 2; Length 28;

Best Local Similarity 100.0%; Pred. No. 1.1e+04;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 IQL 7

|||

Db 3 IQL 5

RESULT 32

B60071

vasoactive intestinal peptide - rhesus macaque

C;Species: Macaca mulatta (rhesus macaque)

C;Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 20-Mar-1998

C;Accession: B60071

R;Yu, J.; Xin, Y.; Eng, J.; Yalow, R.S.

Regul. Pept. 32, 39-45, 1991

A;Title: Rhesus monkey gastroenteropancreatic hormones: relationship to human sequences.

A;Reference number: A60071; MUID:91164506; PMID:2003150

A;Accession: B60071

A;Status: protein sequence not shown

A;Molecule type: protein

A;Residues: 1-28 <YUA>

A;Note: the sequence is identical with the human sequence

C;Superfamily: glucagon

C;Keywords: duplication; hormone; intestine; neuropeptide; vasodilator

Query Match 8.8%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
|||
Db 23 LNS 25

RESULT 33

A60304

vasoactive intestinal peptide - dog

N;Alternate names: VIP

C;Species: Canis lupus familiaris (dog)

C;Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 20-Mar-1998

C;Accession: A60304

R;Eng, J.; Pan, Y.C.E.; Raufman, J.P.; Yalow, R.S.

Regul. Pept. Suppl. 3, S14, 1985

A;Title: Purification and sequencing of dog and guinea pig VIP's.

A;Reference number: A60304

A;Accession: A60304

A;Molecule type: protein

A;Residues: 1-28 <ENG>

C;Superfamily: glucagon

C;Keywords: duplication; hormone; intestine; neuropeptide; vasodilator

Query Match 8.8%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
|||
Db 23 LNS 25

RESULT 34

S58386

T-cell receptor beta-chain Vb11-Jb2.4 - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 29-Nov-1995 #sequence_revision 01-Mar-1996 #text_change 23-Jul-1999

C;Accession: S58386
 R;Johnston, S.L.; Strausbauch, M.; Sarkar, G.; Wettstein, P.J.
 Nucleic Acids Res. 23, 3074-3075, 1995
 A;Title: A novel method for sequencing members of multi-gene families.
 A;Reference number: S58384; MUID:95388532; PMID:7659534
 A;Accession: S58386
 A;Status: preliminary; nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 1-28 <JOH>
 A;Cross-references: EMBL:U20300; NID:g663123; PIDN:AAA62247.1; PID:g663124
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1995
 A;Note: only a part of the coding sequence is given
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: T-cell receptor

Query Match 8.8%; Score 3; DB 2; Length 28;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 ERV 21
 |||
 Db 12 ERV 14

RESULT 35

S56121
 type I DNA methyltransferase M.EcoR124I chain HsdS - Escherichia coli
 (fragments)
 C;Species: Escherichia coli
 C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 03-Nov-1995
 C;Accession: S56121
 R;Webb, M.; Taylor, I.A.; Firman, K.; Kneale, G.G.
 J. Mol. Biol. 250, 181-190, 1995
 A;Title: Probing the domain structure of the type IC DNA methyltransferase
 M.EcoR124I by limited proteolysis.
 A;Reference number: S56121; MUID:95333175; PMID:7608969
 A;Accession: S56121
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-28 <WEB>

Query Match 8.8%; Score 3; DB 2; Length 28;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 30 DVH 32
 |||
 Db 8 DVH 10

RESULT 36

S70894
 hypothetical protein 1 - Vibrio anguillarum (fragment)
 C;Species: Vibrio anguillarum
 C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
 C;Accession: S70894

R;O'Toole, R.; Milton, D.L.; Wolf-Watz, H.

Mol. Microbiol. 19, 625-637, 1996

A;Title: Chemotactic motility is required for invasion of the host by the fish pathogen *Vibrio anguillarum*.

A;Reference number: S70894; MUID:96228710; PMID:8830252

A;Accession: S70894

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-28 <OTO>

A;Cross-references: GB:U36378; EMBL:L47344; NID:g1020321; PIDN:AAB38488.1; PID:g1723992

Query Match 8.8%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
|||
Db 18 LNS 20

RESULT 37

S22469

hypothetical protein 1 - *Prochlorothrix hollandica*

C;Species: *Prochlorothrix hollandica*

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 15-Oct-1999

C;Accession: S22469; S16850

R;Greer, K.L.; Golden, S.S.

Plant Mol. Biol. 19, 355-365, 1992

A;Title: Conserved relationship between psbH and petBD genes: presence of a shared upstream element in *Prochlorothrix hollandica*.

A;Reference number: S22469; MUID:92322967; PMID:1623188

A;Accession: S22469

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-28 <GRE>

A;Cross-references: EMBL:X60313; NID:g45528; PIDN:CAA42858.1; PID:g45529

Query Match 8.8%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVS 3
|||
Db 4 SVS 6

RESULT 38

S26254

rel protein - chicken

C;Species: *Gallus gallus* (chicken)

C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 06-Dec-1996

C;Accession: S26254

R;Capobianco, A.J.; Gilmore, T.D.

Oncogene 6, 2203-2210, 1991

A;Title: Repression of the chicken c-rel promoter by vRel in chicken embryo fibroblasts is not mediated through a consensus NF-kappaB binding site.

A;Reference number: S26254; MUID:92115319; PMID:1766669
A;Accession: S26254
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-28 <CAP>
A;Cross-references: EMBL:X59588

Query Match 8.8%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 RVE 22
|||
Db 1 RVE 3

RESULT 39

I59477

antigen, T-cell receptor - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jul-2000

C;Accession: I59477

R;Mathioudakis, G.; Chen, P.

Scand. J. Immunol. 38, 31-36, 1993

A;Title: Preferential rearrangements of the V gamma I subgroup of the gamma-chain of the T-cell antigen receptor to J gamma 2C gamma 2 gene segments in peripheral blood lymphocyte transcripts from normal donors.

A;Reference number: I59477; MUID:93318104; PMID:8392223

A;Accession: I59477

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-28 <RES>

A;Cross-references: GB:M89844; NID:g181657; PIDN:AAA02695.1; PID:g181658

C;Keywords: T-cell receptor

Query Match 8.8%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKL 28
|||
Db 10 KKL 12

RESULT 40

F46522

T-cell receptor eta chain - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999

C;Accession: F46522; I56191

R;Jensen, J.P.; Cenciarelli, C.; Hou, D.; Rellahan, B.L.; Dean, M.; Weissman, A.M.

J. Immunol. 150, 122-130, 1993

A;Title: T cell antigen receptor-eta subunit. Low levels of expression and limited cross-species conservation.

A;Reference number: A46522; MUID:93107707; PMID:8417118

A;Accession: F46522

A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-28 <JEN>
A;Cross-references: GB:S51404; NID:g262180; PIDN:AAB24606.1; PID:g262181
A;Note: sequence extracted from NCBI backbone (NCBIP:120909)
R;Itoh, Y.; Matsuura, A.; Kinebuchi, M.; Honda, R.; Takayama, S.; Ichimiya, S.;
Kon, S.; Kikuchi, K.
J. Immunol. 151, 4705-4717, 1993
A;Title: Structural analysis of the CD3 zeta/eta locus of the rat. Expression of
zeta but eta transcripts by rat T cells.
A;Reference number: I56191; MUID:94014415; PMID:8409430
A;Accession: I56191
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-28 <RES>
A;Cross-references: GB:D13556; NID:g436580; PIDN:BAA02754.1; PID:g436581
C;Keywords: T-cell receptor

Query Match 8.8%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 25 RKK 27
|||
Db 13 RKK 15

Search completed: January 14, 2004, 10:37:22
Job time : 12.0623 secs

OM protein - protein search, using sw model

Run on: January 14, 2004, 10:37:44 ; Search time 22.8785 Seconds
(without alignments)
303.882 Million cell updates/sec

Title: US-09-843-221A-162
Perfect score: 34
Sequence: 1 SVSEIQLMHNRGKHLNSMERVEWLRKKLQDVHNF 34

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 762491 seqs, 204481190 residues

Word size : 0

Total number of hits satisfying chosen parameters: 28045

Minimum DB seq length: 28
Maximum DB seq length: 40

Post-processing: Listing first 1000 summaries

Database : Published_Applications_AA:*

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8	23	67.6	34	11	US-09-843-221A-18	Sequence 18, Appl
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264	4	11.8	35	11	US-09-820-843A-106	Sequence 106, App
265	4	11.8	35	11	US-09-925-299-1258	Sequence 1258, Ap
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819	3	8.8	28	15	US-10-023-282-626	Sequence 626, App
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822	3	8.8	28	15	US-10-023-282-1089	Sequence 1089, Ap
823	3	8.8	28	15	US-10-255-532-6	Sequence 6, Appli
824	3	8.8	28	15	US-10-075-869-24	Sequence 24, Appl
825	3	8.8	28	15	US-10-202-724-3	Sequence 3, Appli
826	3	8.8	28	15	US-10-262-017-3	Sequence 3, Appli
827	3	8.8	28	15	US-10-106-698-5608	Sequence 5608, Ap
828	3	8.8	28	15	US-10-106-698-6764	Sequence 6764, Ap
829	3	8.8	28	15	US-10-106-698-7736	Sequence 7736, Ap
830	3	8.8	28	15	US-10-106-698-7875	Sequence 7875, Ap
831	3	8.8	28	15	US-10-106-698-8447	Sequence 8447, Ap
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833	3	8.8	28	15	US-10-197-954-62	Sequence 62, Appl
834	3	8.8	28	15	US-10-197-954-145	Sequence 145, App
835	3	8.8	28	15	US-10-283-500-19	Sequence 19, Appl
836	3	8.8	28	15	US-10-295-981-23	Sequence 23, Appl
837	3	8.8	28	15	US-10-160-290-22	Sequence 22, Appl
838	3	8.8	29	9	US-09-730-379B-4	Sequence 4, Appli
839	3	8.8	29	9	US-09-765-527-13	Sequence 13, Appl
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843	3	8.8	29	9	US-09-224-683-73	Sequence 73, Appl
844	3	8.8	29	9	US-09-932-161-1	Sequence 1, Appli
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848	3	8.8	29	9	US-09-864-761-35314	Sequence 35314, A
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874	3	8.8	29	9	US-09-864-761-45036	Sequence 45036, A
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878	3	8.8	29	9	US-09-864-761-46618	Sequence 46618, A
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887	3	8.8	29	9	US-09-925-299-1270	Sequence 1270, Ap
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899	3	8.8	29	10	US-09-908-664-9	Sequence 9, Appli
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904	3	8.8	29	10	US-09-003-869-98	Sequence 98, Appl
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907	3	8.8	29	10	US-09-880-149-55	Sequence 55, Appl
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918	3	8.8	29	11	US-09-974-879-527	Sequence 527, App
919	3	8.8	29	11	US-09-259-658-15	Sequence 15, Appl
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922	3	8.8	29	11	US-09-843-221A-152	Sequence 152, App
923	3	8.8	29	11	US-09-925-299-1270	Sequence 1270, Ap
924	3	8.8	29	11	US-09-847-102A-80	Sequence 80, Appl
925	3	8.8	29	11	US-09-813-153-218	Sequence 218, App
926	3	8.8	29	11	US-09-966-262-227	Sequence 227, App
927	3	8.8	29	11	US-09-969-730-196	Sequence 196, App
928	3	8.8	29	11	US-09-983-966-227	Sequence 227, App
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932	3	8.8	29	11	US-09-892-877-436	Sequence 436, App
933	3	8.8	29	11	US-09-847-208-125	Sequence 125, App
934	3	8.8	29	11	US-09-305-736-406	Sequence 406, App
935	3	8.8	29	11	US-09-305-736-512	Sequence 512, App
936	3	8.8	29	11	US-09-305-736-529	Sequence 529, App
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938	3	8.8	29	11	US-09-095-478-25	Sequence 25, Appl
939	3	8.8	29	11	US-09-908-139-19	Sequence 19, Appl
940	3	8.8	29	11	US-09-908-139-21	Sequence 21, Appl
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942	3	8.8	29	11	US-09-491-614-15	Sequence 15, Appl
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944	3	8.8	29	11	US-09-910-082A-73	Sequence 73, Appl
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946	3	8.8	29	11	US-09-910-082A-85	Sequence 85, Appl
947	3	8.8	29	11	US-09-910-082A-158	Sequence 158, App
948	3	8.8	29	11	US-09-910-082A-368	Sequence 368, App
949	3	8.8	29	12	US-10-153-604A-72	Sequence 72, Appl
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951	3	8.8	29	12	US-10-345-281-52	Sequence 52, Appl
952	3	8.8	29	12	US-10-345-281-55	Sequence 55, Appl
953	3	8.8	29	12	US-10-234-816-95	Sequence 95, Appl
954	3	8.8	29	12	US-09-789-831-13	Sequence 13, Appl
955	3	8.8	29	12	US-09-935-384-757	Sequence 757, App
956	3	8.8	29	12	US-09-935-384-758	Sequence 758, App
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958	3	8.8	29	12	US-10-096-777-1	Sequence 1, Appli
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960	3	8.8	29	12	US-10-008-524A-123	Sequence. 123, App
961	3	8.8	29	12	US-10-340-458-4	Sequence 4, Appli
962	3	8.8	29	12	US-10-340-458-21	Sequence 21, Appl
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964	3	8.8	29	12	US-10-105-232-319	Sequence 319, App
965	3	8.8	29	12	US-10-105-232-512	Sequence 512, App
966	3	8.8	29	12	US-10-280-066-334	Sequence 334, App
967	3	8.8	29	12	US-10-289-135A-25	Sequence 25, Appl
968	3	8.8	29	12	US-10-263-162-6	Sequence 6, Appli

969	3	8.8	29	12	US-10-351-641-88	Sequence 88, Appl
970	3	8.8	29	12	US-09-962-756-1344	Sequence 1344, Ap
971	3	8.8	29	12	US-09-962-756-1370	Sequence 1370, Ap
972	3	8.8	29	12	US-09-962-756-1380	Sequence 1380, Ap
973	3	8.8	29	12	US-09-962-756-1382	Sequence 1382, Ap
974	3	8.8	29	12	US-09-962-756-1385	Sequence 1385, Ap
975	3	8.8	29	12	US-09-962-756-1389	Sequence 1389, Ap
976	3	8.8	29	12	US-09-962-756-1392	Sequence 1392, Ap
977	3	8.8	29	12	US-09-962-756-1394	Sequence 1394, Ap
978	3	8.8	29	12	US-09-962-756-1400	Sequence 1400, Ap
979	3	8.8	29	12	US-09-962-756-1406	Sequence 1406, Ap
980	3	8.8	29	12	US-09-962-756-1411	Sequence 1411, Ap
981	3	8.8	29	12	US-09-962-756-1414	Sequence 1414, Ap
982	3	8.8	29	12	US-09-962-756-1419	Sequence 1419, Ap
983	3	8.8	29	12	US-09-962-756-1420	Sequence 1420, Ap
984	3	8.8	29	12	US-09-962-756-1430	Sequence 1430, Ap
985	3	8.8	29	12	US-10-029-386-27545	Sequence 27545, A
986	3	8.8	29	12	US-10-029-386-27896	Sequence 27896, A
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988	3	8.8	29	12	US-10-029-386-29238	Sequence 29238, A
989	3	8.8	29	12	US-10-029-386-30063	Sequence 30063, A
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991	3	8.8	29	12	US-10-029-386-31577	Sequence 31577, A
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993	3	8.8	29	12	US-10-029-386-32812	Sequence 32812, A
994	3	8.8	29	12	US-10-029-386-33620	Sequence 33620, A
995	3	8.8	29	12	US-10-189-437-306	Sequence 306, App
996	3	8.8	29	12	US-10-189-437-499	Sequence 499, App
997	3	8.8	29	12	US-10-189-437-641	Sequence 641, App
998	3	8.8	29	12	US-10-189-437-693	Sequence 693, App
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ALIGNMENTS

RESULT 1

US-09-843-221A-17

; Sequence 17, Application US/09843221A

; Publication No. US20030039654A1

; GENERAL INFORMATION:

; APPLICANT: KOSTENUIK, PAUL

; APPLICANT: LIU, CHUAN-FA

; APPLICANT: LACEY, DAVID LEE

; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-

; TITLE OF INVENTION: RELATED PROTEIN

; FILE REFERENCE: A-665B

; CURRENT APPLICATION NUMBER: US/09/843,221A

; CURRENT FILING DATE: 2001-04-26

; PRIOR APPLICATION NUMBER: 60/266,673

; PRIOR FILING DATE: 2001-02-06

; PRIOR APPLICATION NUMBER: 60/214,860

; PRIOR FILING DATE: 2000-06-28

; PRIOR APPLICATION NUMBER: 60/200,053

; PRIOR FILING DATE: 2000-04-27

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; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTH
US-09-843-221A-17
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Query Match 100.0%; Score 34; DB 11; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.6e-28;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 SVSEIQLMHNRGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 2

US-09-843-221A-162

; Sequence 162, Application US/09843221A

; Publication No. US20030039654A1

; GENERAL INFORMATION:

APPLICANT: KOSTENUIK, PAUL

; APPLICANT: LIU, CHUAN-FA

; APPLICANT: LACEY, DAVID LEE

; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND

PARATHYROID HORMONE-

; TITLE OF INVENTION: RELATED PROTEIN

; FILE REFERENCE: A-665B

; CURRENT APPLICATION NUMBER: US/09/843,221A

; CURRENT FILING DATE: 2001-04-26

; PRIOR APPLICATION NUMBER: 60/266,673

; PRIOR FILING DATE: 2001-02-06

; PRIOR APPLICATION NUMBER: 60/214,860

; PRIOR FILING DATE: 2000-06-28

; PRIOR APPLICATION NUMBER: 60/200,053

; PRIOR FILING DATE: 2000-04-27

; NUMBER OF SEQ ID NOS: 170

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; SOFTWARE: PatentIn version 3.1
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; SEQ ID NO 162

; LENGTH: 34

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

OTHER INFORMATION: Preferred embodiments - PTH

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; NAME/KEY: misc_feature
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; LOCATION: (34) .. (34)

; OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus

US-09-843-221A-162

Query Match 100.0%; Score 34; DB 11; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.6e-28;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db

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1 SVSEIQLMHNRGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 3

US-09-843-221A-40

; Sequence 40, Application US/09843221A

; Publication No. US20030039654A1

; GENERAL INFORMATION:

; APPLICANT: KOSTENUIK, PAUL

; APPLICANT: LIU, CHUAN-FA

; APPLICANT: LACEY, DAVID LEE

; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID HORMONE-

; TITLE OF INVENTION: RELATED PROTEIN

; FILE REFERENCE: A-665B

; CURRENT APPLICATION NUMBER: US/09/843,221A

; CURRENT FILING DATE: 2001-04-26

; PRIOR APPLICATION NUMBER: 60/266,673

; PRIOR FILING DATE: 2001-02-06

; PRIOR APPLICATION NUMBER: 60/214,860

; PRIOR FILING DATE: 2000-06-28

; PRIOR APPLICATION NUMBER: 60/200,053

; PRIOR FILING DATE: 2000-04-27

; NUMBER OF SEQ ID NOS: 170

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 40

; LENGTH: 30

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: modified human PTH

US-09-843-221A-40

Query Match 88.2%; Score 30; DB 11; Length 30;

Best Local Similarity 100.0%; Pred. No. 3.3e-24;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 SVSEIQLMHNRGKHLNSMERVEWLRKKLQD 30

RESULT 4

US-09-843-221A-32

; Sequence 32, Application US/09843221A

; Publication No. US20030039654A1

; GENERAL INFORMATION:

; APPLICANT: KOSTENUIK, PAUL

; APPLICANT: LIU, CHUAN-FA

; APPLICANT: LACEY, DAVID LEE

; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID HORMONE-

; TITLE OF INVENTION: RELATED PROTEIN

; FILE REFERENCE: A-665B

; CURRENT APPLICATION NUMBER: US/09/843,221A

; CURRENT FILING DATE: 2001-04-26

; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-843-221A-32

Query Match 67.6%; Score 23; DB 11; Length 28;
Best Local Similarity 100.0%; Pred. No. 5.7e-17;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||
Db 6 GKHLNSMERVEWLRKKLQDVHNF 28

RESULT 5

US-09-169-786-3
; Sequence 3, Application US/09169786B
; Patent No. US20020025929A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Masahiko
; TITLE OF INVENTION: METHOD OF BUILDING AND MAINTAINING BONE
; FILE REFERENCE: X-11480
; CURRENT APPLICATION NUMBER: US/09/169,786B
; CURRENT FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 60/061,800
; EARLIER FILING DATE: 1997-10-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-169-786-3

Query Match 67.6%; Score 23; DB 9; Length 34;
Best Local Similarity 100.0%; Pred. No. 6.6e-17;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
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Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 6

US-09-928-047B-6
; Sequence 6, Application US/09928047B
; Patent No. US20020160945A1
; GENERAL INFORMATION:

; APPLICANT: Cantor, Thomas
; TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE
; TITLE OF INVENTION: ANTAGONIST OR MODULATORS AND OSTEOPOROSIS
; FILE REFERENCE: 53221-20002.00
; CURRENT APPLICATION NUMBER: US/09/928,047B
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/224,446
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-928-047B-6

Query Match 67.6%; Score 23; DB 10; Length 34;
Best Local Similarity 100.0%; Pred. No. 6.6e-17;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
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Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 7

US-09-843-221A-16
; Sequence 16, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-843-221A-16

Query Match 67.6%; Score 23; DB 11; Length 34;
Best Local Similarity 100.0%; Pred. No. 6.6e-17;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
| | | | | | | | | | | | | | | | | |
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 8

US-09-843-221A-18
; Sequence 18, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTH
US-09-843-221A-18

Query Match 67.6%; Score 23; DB 11; Length 34;
Best Local Similarity 100.0%; Pred. No. 6.6e-17;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
| | | | | | | | | | | | | | | | | |
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 9

US-09-843-221A-20
; Sequence 20, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A

```
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
;   LENGTH: 34
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: modified human PTH
US-09-843-221A-20
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Query Match          67.6%; Score 23; DB 11; Length 34;
Best Local Similarity 100.0%; Pred. No. 6.6e-17;
Matches    23; Conservative    0; Mismatches    0; Indels    0; Gaps    0;
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Qy      12 GKHLNSMERVEWLRKKLQDVHNF 34
          |||
Db      12 GKHLNSMERVEWLRKKLQDVHNF 34
```

RESULT 10

US-09-843-221A-161

```
; Sequence 161, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 161
;   LENGTH: 34
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Preferred embodiments - PTH
; NAME/KEY: misc_feature
; LOCATION: (34)..(34)
; OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus
```

US-09-843-221A-161

Query Match 67.6%; Score 23; DB 11; Length 34;
Best Local Similarity 100.0%; Pred. No. 6.6e-17;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 11

US-09-843-221A-163

; Sequence 163, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 163
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Preferred embodiments - PTH
; NAME/KEY: misc_feature
; LOCATION: (34)..(34)
; OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus
US-09-843-221A-163

Query Match 67.6%; Score 23; DB 11; Length 34;
Best Local Similarity 100.0%; Pred. No. 6.6e-17;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 12

US-09-928-048A-6

; Sequence 6, Application US/09928048A
; Publication No. US20030138858A1

; GENERAL INFORMATION:
; APPLICANT: Scantibodies Laboratory, Inc.
; APPLICANT: Cantor, Thomas L.
; TITLE OF INVENTION: METHODS AND DEVICES FOR DIRECT
; TITLE OF INVENTION: DETERMINATION OF CYCLASE INHIBITING PARATHYROID HORMONE
; FILE REFERENCE: 53221-20015.00
; CURRENT APPLICATION NUMBER: US/09/928,048A
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-928-048A-6

Query Match 67.6%; Score 23; DB 12; Length 34;
Best Local Similarity 100.0%; Pred. No. 6.6e-17;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 13

US-10-361-928-1

; Sequence 1, Application US/10361928
; Publication No. US20030144209A1
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: ANALOGS
; FILE REFERENCE: 0609.4630002
; CURRENT APPLICATION NUMBER: US/10/361,928
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: 09/447,800
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 60/110,152
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (1)
; OTHER INFORMATION: Can be desamino Ser, desamino Ala, or desamino Gly
US-10-361-928-1

Query Match 67.6%; Score 23; DB 12; Length 34;
Best Local Similarity 100.0%; Pred. No. 6.6e-17;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
| | | | | | | | | | | | | | | | | |
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 14

US-10-361-928-2

; Sequence 2, Application US/10361928
; Publication No. US20030144209A1
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: ANALOGS
; FILE REFERENCE: 0609.4630002
; CURRENT APPLICATION NUMBER: US/10/361,928
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: 09/447,800
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 60/110,152
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Desamino Gly

US-10-361-928-2

Query Match 67.6%; Score 23; DB 12; Length 34;
Best Local Similarity 100.0%; Pred. No. 6.6e-17;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
| | | | | | | | | | | | | | | | | |
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 15

US-10-361-928-5

; Sequence 5, Application US/10361928
; Publication No. US20030144209A1
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: ANALOGS
; FILE REFERENCE: 0609.4630002
; CURRENT APPLICATION NUMBER: US/10/361,928
; CURRENT FILING DATE: 2003-02-11

; PRIOR APPLICATION NUMBER: 09/447,800
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 60/110,152
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Desamino Ala
US-10-361-928-5

Query Match 67.6%; Score 23; DB 12; Length 34;
Best Local Similarity 100.0%; Pred. No. 6.6e-17;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 16

US-10-361-928-8

; Sequence 8, Application US/10361928
; Publication No. US20030144209A1
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: ANALOGS
; FILE REFERENCE: 0609.4630002
; CURRENT APPLICATION NUMBER: US/10/361,928
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: 09/447,800
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 60/110,152
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Desamino Ser
US-10-361-928-8

Query Match 67.6%; Score 23; DB 12; Length 34;
Best Local Similarity 100.0%; Pred. No. 6.6e-17;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
| | | | | | | | | | | | | | | | | |
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 17

US-10-340-484-15

; Sequence 15, Application US/10340484
; Publication No. US20030171288A1
; GENERAL INFORMATION:
; APPLICANT: Stewart, Andrew F.
; TITLE OF INVENTION: Treatment of Bone Disorders with Skelatal Anabolic
; TITLE OF INVENTION: Drugs
; FILE REFERENCE: 25200-501
; CURRENT APPLICATION NUMBER: US/10/340,484
; CURRENT FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: 60/347,215
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: 60/353,296
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 60/368,955
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: 60/379,125
; PRIOR FILING DATE: 2002-05-08
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-340-484-15

Query Match 67.6%; Score 23; DB 12; Length 34;
Best Local Similarity 100.0%; Pred. No. 6.6e-17;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
| | | | | | | | | | | | | | | | | |
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 18

US-10-340-484-16

; Sequence 16, Application US/10340484
; Publication No. US20030171288A1
; GENERAL INFORMATION:
; APPLICANT: Stewart, Andrew F.
; TITLE OF INVENTION: Treatment of Bone Disorders with Skelatal Anabolic
; TITLE OF INVENTION: Drugs
; FILE REFERENCE: 25200-501
; CURRENT APPLICATION NUMBER: US/10/340,484
; CURRENT FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: 60/347,215
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: 60/353,296
; PRIOR FILING DATE: 2002-02-01

; PRIOR APPLICATION NUMBER: 60/368,955
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: 60/379,125
; PRIOR FILING DATE: 2002-05-08
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Macaca fascicularis
US-10-340-484-16

Query Match 67.6%; Score 23; DB 12; Length 34;
Best Local Similarity 100.0%; Pred. No. 6.6e-17;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34
| | | | | | | | | | | | | | | | | |
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 19

US-10-016-403-5

; Sequence 5, Application US/10016403
; Publication No. US20020107505A1

; GENERAL INFORMATION:

; APPLICANT: Holladay, Leslie A.

; TITLE OF INVENTION: MODIFICATION OF POLYPEPTIDE DRUGS TO
; INCREASE ELECTROTRANSPORT FLUX

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Stroud, Stroud, Willink, Thompson & Howard

; STREET: 25 West Main Street

; CITY: Madison

; STATE: WI

; COUNTRY: USA

; ZIP: 53701-2236

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/016,403

; FILING DATE: 10-Dec-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/466,610

; FILING DATE: 1995-JUN-06

; ATTORNEY/AGENT INFORMATION:

; NAME: Frenchick, Grady J.

; REGISTRATION NUMBER: 29,018

; REFERENCE/DOCKET NUMBER: 8734.28

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 608-257-2281

; TELEFAX: 608-257-7643

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..34
; OTHER INFORMATION: /note= "parathyroid hormone"
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-016-403-5

Query Match 67.6%; Score 23; DB 14; Length 34;
Best Local Similarity 100.0%; Pred. No. 6.6e-17;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 20

US-10-016-403-6

; Sequence 6, Application US/10016403
; Publication No. US20020107505A1

; GENERAL INFORMATION:

; APPLICANT: Holladay, Leslie A.

; TITLE OF INVENTION: MODIFICATION OF POLYPEPTIDE DRUGS TO
; INCREASE ELECTROTRANSPORT FLUX

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Stroud, Stroud, Willink, Thompson & Howard

; STREET: 25 West Main Street

; CITY: Madison

; STATE: WI

; COUNTRY: USA

; ZIP: 53701-2236

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/016,403

; FILING DATE: 10-Dec-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/466,610

; FILING DATE: 1995-JUN-06

; ATTORNEY/AGENT INFORMATION:

; NAME: Frenchick, Grady J.

; REGISTRATION NUMBER: 29,018

; REFERENCE/DOCKET NUMBER: 8734.28

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 608-257-2281

; TELEFAX: 608-257-7643

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..34
; OTHER INFORMATION: /note= "modified parathyroid
; hormone"
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-016-403-6

Query Match 67.6%; Score 23; DB 14; Length 34;
Best Local Similarity 100.0%; Pred. No. 6.6e-17;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 21

US-10-097-079-1

; Sequence 1, Application US/10097079

; Publication No. US20020132973A1

; GENERAL INFORMATION:

; APPLICANT: Condon, Stephen M.

; Morize, Isabelle

; TITLE OF INVENTION: PEPTIDE PARATHYROID HORMONE ANALOGS

; NUMBER OF SEQUENCES: 88

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Rhone-Poulenc Rorer Inc.

; STREET: 500 Arcola Road, Mailstop 3C43

; CITY: Collegeville

; STATE: PA

; COUNTRY: USA

; ZIP: 19426

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/097,079

; FILING DATE: 13-Mar-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/228,990

; FILING DATE: <Unknown>

; APPLICATION NUMBER: US 60/046,472

; FILING DATE: 14-MAY-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Martin Esq., Michael B.

; REGISTRATION NUMBER: 37,521

; REFERENCE/DOCKET NUMBER: A2678B-WO

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (610) 454-2793

; TELEFAX: (610) 454-3808

RESULT 23

US-10-168-185-9

; Sequence 9, Application US/10168185
 ; Publication No. US20030175802A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Armbruster, Franz Paul
 ; APPLICANT: Missbichler, Albert
 ; APPLICANT: Schmidt-Gayk, Heinrich
 ; APPLICANT: Roth, Heinz-Jurgen
 ; TITLE OF INVENTION: Method for Determining Parathormone
 ; TITLE OF INVENTION: Activity in a Human Sample
 ; FILE REFERENCE: HLZ-004US
 ; CURRENT APPLICATION NUMBER: US/10/168,185
 ; CURRENT FILING DATE: 2002-06-17
 ; PRIOR APPLICATION NUMBER: PCT/EP00/12911
 ; PRIOR FILING DATE: 2000-12-18
 ; PRIOR APPLICATION NUMBER: DE 19961350
 ; PRIOR FILING DATE: 1999-12-17
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 9
 ; LENGTH: 37
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

US-10-168-185-9

Query Match 67.6%; Score 23; DB 12; Length 37;
 Best Local Similarity 100.0%; Pred. No. 7.1e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 24

US-09-169-786-4

; Sequence 4, Application US/09169786B
 ; Patent No. US20020025929A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sato, Masahiko
 ; TITLE OF INVENTION: METHOD OF BUILDING AND MAINTAINING BONE
 ; FILE REFERENCE: X-11480
 ; CURRENT APPLICATION NUMBER: US/09/169,786B
 ; CURRENT FILING DATE: 1998-10-09
 ; EARLIER APPLICATION NUMBER: US 60/061,800
 ; EARLIER FILING DATE: 1997-10-14
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 4
 ; LENGTH: 38
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

US-09-169-786-4

Query Match 67.6%; Score 23; DB 9; Length 38;
 Best Local Similarity 100.0%; Pred. No. 7.2e-17;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 25

US-09-843-221A-14

; Sequence 14, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-843-221A-14

Query Match 67.6%; Score 23; DB 11; Length 38;
Best Local Similarity 100.0%; Pred. No. 7.2e-17;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 26

US-10-245-707-1

; Sequence 1, Application US/10245707
; Publication No. US20030171282A1
; GENERAL INFORMATION:
; APPLICANT: Patton, John S.
; TITLE OF INVENTION: Pulmonary Delivery of Active Fragments of Parathyroid
Hormone
; FILE REFERENCE: 032055-047
; CURRENT APPLICATION NUMBER: US/10/245,707
; CURRENT FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 09/577,264
; PRIOR FILING DATE: 2000-05-22


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; PRIOR APPLICATION NUMBER: US 09/128,401
; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: US 08/625,586
; PRIOR FILING DATE: 1996-03-28
; PRIOR APPLICATION NUMBER: US 08/232,849
; PRIOR FILING DATE: 1994-04-25
; PRIOR APPLICATION NUMBER: US 07/953,397
; PRIOR FILING DATE: 1992-09-29
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 38
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: parathyroid hormone (PTH) fragment molecules
US-10-245-707-1

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Query Match          67.6%; Score 23; DB 12; Length 38;
Best Local Similarity 100.0%; Pred. No. 7.2e-17;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      12 GKHLNSMERVEWLRKKLQDVHNF 34
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Db      12 GKHLNSMERVEWLRKKLQDVHNF 34

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RESULT 27

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US-10-361-928-3
; Sequence 3, Application US/10361928
; Publication No. US20030144209A1
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: ANALOGS
; FILE REFERENCE: 0609.4630002
; CURRENT APPLICATION NUMBER: US/10/361,928
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: 09/447,800
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 60/110,152
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 33
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (1)
;   OTHER INFORMATION: Desamino Gly
US-10-361-928-3

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```

Query Match          64.7%; Score 22; DB 12; Length 33;

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Best Local Similarity 100.0%; Pred. No. 7e-16;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHN 33
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Db 12 GKHLNSMERVEWLRKKLQDVHN 33

RESULT 28

US-10-361-928-6

; Sequence 6, Application US/10361928
; Publication No. US20030144209A1
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: ANALOGS
; FILE REFERENCE: 0609.4630002
; CURRENT APPLICATION NUMBER: US/10/361,928
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: 09/447,800
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 60/110,152
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Desamino Ala
US-10-361-928-6

Query Match 64.7%; Score 22; DB 12; Length 33;
Best Local Similarity 100.0%; Pred. No. 7e-16;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHN 33
 |||||
Db 12 GKHLNSMERVEWLRKKLQDVHN 33

RESULT 29

US-10-361-928-9

; Sequence 9, Application US/10361928
; Publication No. US20030144209A1
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: ANALOGS
; FILE REFERENCE: 0609.4630002

RESULT 31

US-09-169-786-2

; Sequence 2, Application US/09169786B
 ; Patent No. US20020025929A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sato, Masahiko
 ; TITLE OF INVENTION: METHOD OF BUILDING AND MAINTAINING BONE
 ; FILE REFERENCE: X-11480
 ; CURRENT APPLICATION NUMBER: US/09/169,786B
 ; CURRENT FILING DATE: 1998-10-09
 ; EARLIER APPLICATION NUMBER: US 60/061,800
 ; EARLIER FILING DATE: 1997-10-14
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 31
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-169-786-2

Query Match 58.8%; Score 20; DB 9; Length 31;
 Best Local Similarity 100.0%; Pred. No. 7.9e-14;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDV 31
 |||||
 Db 12 GKHLNSMERVEWLRKKLQDV 31

RESULT 32

US-09-843-221A-27

; Sequence 27, Application US/09843221A
 ; Publication No. US20030039654A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KOSTENUIK, PAUL
 ; APPLICANT: LIU, CHUAN-FA
 ; APPLICANT: LACEY, DAVID LEE
 ; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
 PARATHYROID HORMONE-
 ; TITLE OF INVENTION: RELATED PROTEIN
 ; FILE REFERENCE: A-665B
 ; CURRENT APPLICATION NUMBER: US/09/843,221A
 ; CURRENT FILING DATE: 2001-04-26
 ; PRIOR APPLICATION NUMBER: 60/266,673
 ; PRIOR FILING DATE: 2001-02-06
 ; PRIOR APPLICATION NUMBER: 60/214,860
 ; PRIOR FILING DATE: 2000-06-28
 ; PRIOR APPLICATION NUMBER: 60/200,053
 ; PRIOR FILING DATE: 2000-04-27
 ; NUMBER OF SEQ ID NOS: 170
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 27
 ; LENGTH: 31
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

US-09-843-221A-27

Query Match 58.8%; Score 20; DB 11; Length 31;
Best Local Similarity 100.0%; Pred. No. 7.9e-14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDV 31
|||||
Db 12 GKHLNSMERVEWLRKKLQDV 31

RESULT 33

US-09-843-221A-165

; Sequence 165, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 165
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Preferred embodiments - PTH
; NAME/KEY: misc_feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus
US-09-843-221A-165

Query Match 58.8%; Score 20; DB 11; Length 31;
Best Local Similarity 100.0%; Pred. No. 7.9e-14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDV 31
|||||
Db 12 GKHLNSMERVEWLRKKLQDV 31

RESULT 34

US-09-843-221A-39

; Sequence 39, Application US/09843221A
; Publication No. US20030039654A1

```

; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-843-221A-39

```

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Query Match          55.9%; Score 19; DB 11; Length 30;
Best Local Similarity 100.0%; Pred. No. 8.4e-13;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      12 GKHLNSMERVEWLRKKLQD 30
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Db      12 GKHLNSMERVEWLRKKLQD 30

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RESULT 35

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US-09-843-221A-41
; Sequence 41, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 41
; LENGTH: 30

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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTH
US-09-843-221A-41

Query Match 55.9%; Score 19; DB 11; Length 30;
Best Local Similarity 100.0%; Pred. No. 8.4e-13;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQD 30
|||
Db 12 GKHLNSMERVEWLRKKLQD 30

RESULT 36

US-09-843-221A-43

; Sequence 43, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTH
US-09-843-221A-43

Query Match 55.9%; Score 19; DB 11; Length 30;
Best Local Similarity 100.0%; Pred. No. 8.4e-13;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQD 30
|||
Db 12 GKHLNSMERVEWLRKKLQD 30

RESULT 37

US-09-843-221A-166

; Sequence 166, Application US/09843221A

; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 166
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Preferred embodiments - PTH
; NAME/KEY: misc_feature
; LOCATION: (30)..(30)
; OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus
US-09-843-221A-166

Query Match 55.9%; Score 19; DB 11; Length 30;
Best Local Similarity 100.0%; Pred. No. 8.4e-13;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQD 30
|||||
Db 12 GKHLNSMERVEWLRKKLQD 30

RESULT 38

US-09-843-221A-34

; Sequence 34, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28

RESULT 40

US-09-843-221A-167

; Sequence 167, Application US/09843221A

; Publication No. US20030039654A1

; GENERAL INFORMATION:

; APPLICANT: KOSTENUK, PAUL

; APPLICANT: LIU, CHUAN-FA

; APPLICANT: LACEY, DAVID LEE

; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-

; TITLE OF INVENTION: RELATED PROTEIN

; FILE REFERENCE: A-665B

; CURRENT APPLICATION NUMBER: US/09/843,221A

; CURRENT FILING DATE: 2001-04-26

; PRIOR APPLICATION NUMBER: 60/266,673

; PRIOR FILING DATE: 2001-02-06

; PRIOR APPLICATION NUMBER: 60/214,860

; PRIOR FILING DATE: 2000-06-28

; PRIOR APPLICATION NUMBER: 60/200,053

; PRIOR FILING DATE: 2000-04-27

; NUMBER OF SEQ ID NOS: 170

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 167

; LENGTH: 29

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Preferred embodiments - PTH

; NAME/KEY: misc_feature

; LOCATION: (1)..(1)

; OTHER INFORMATION: Fc domain attached at the N-terminus through optional
linker

US-09-843-221A-167

Query Match 52.9%; Score 18; DB 11; Length 29;

Best Local Similarity 100.0%; Pred. No. 8.9e-12;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQ 29

|||||

Db 12 GKHLNSMERVEWLRKKLQ 29

Search completed: January 14, 2004, 11:15:03

Job time : 23.8785 secs

OM protein - protein search, using sw model

Run on: January 14, 2004, 10:28:19 ; Search time 25.4206 Seconds
(without alignments)
345.145 Million cell updates/sec

Title: US-09-843-221A-162
Perfect score: 34
Sequence: 1 SVSEIQLMHNRGKHLNSMERVEWLRKKLQDVHNF 34

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 13497

Minimum DB seq length: 28
Maximum DB seq length: 40

Post-processing: Listing first 1000 summaries

Database : SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
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6: sp_mammal:*
7: sp_mhc:*
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9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp Vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query					
No.	Score	Match	Length	DB	ID		Description

1	9	26.5	31	11	Q91Y90	Q91y90 peromyscus
2	9	26.5	31	11	Q91Y91	Q91y91 peromyscus
3	5	14.7	34	5	O17148	O17148 echinococcu
4	5	14.7	34	16	Q97K50	Q97k50 clostridium
5	5	14.7	34	17	Q9HR65	Q9hr65 halobacteri
6	5	14.7	35	11	Q8BTB9	Q8btb9 mus musculu
7	5	14.7	35	16	Q97RG6	Q97rg6 streptococc
8	4	11.8	28	10	O24285	O24285 pinus radia
9	4	11.8	29	2	Q49148	Q49148 methylobact
10	4	11.8	29	4	Q9UCL2	Q9ucl2 homo sapien
11	4	11.8	29	5	Q25603	Q25603 onchocerca
12	4	11.8	29	8	Q9TI61	Q9ti61 allosyncarp
13	4	11.8	29	13	O13043	O13043 scyliorhinu
14	4	11.8	30	4	Q9UBV5	Q9ubv5 homo sapien
15	4	11.8	30	16	Q8DZP7	Q8dzp7 streptococc
16	4	11.8	31	1	Q55314	Q55314 sulfolobus
17	4	11.8	31	4	Q8NEI8	Q8nei8 homo sapien
18	4	11.8	31	16	O50669	O50669 borrelia bu
19	4	11.8	32	11	Q9QZQ2	Q9qzq2 mus musculu
20	4	11.8	32	17	Q9HSZ0	Q9hsz0 halobacteri
21	4	11.8	33	5	Q95SD4	Q95sd4 drosophila
22	4	11.8	33	16	Q9PKX3	Q9pkx3 chlamydia m
23	4	11.8	34	2	Q9ZG81	Q9zgz81 chlamydia t
24	4	11.8	34	2	Q8GFK2	Q8gfk2 staphylococ
25	4	11.8	34	11	Q8C4P4	Q8c4p4 mus musculu
26	4	11.8	34	13	Q90ZJ4	Q90zj4 gallus gall
27	4	11.8	34	16	Q98FK5	Q98fk5 rhizobium l
28	4	11.8	35	4	Q15421	Q15421 homo sapien
29	4	11.8	35	12	Q8V6J8	Q8v6j8 halovirus h
30	4	11.8	35	16	Q9KQG4	Q9kqg4 vibrio chol
31	4	11.8	35	16	Q8F102	Q8f102 leptospira
32	4	11.8	36	2	Q53920	Q53920 streptomyce
33	4	11.8	36	2	O68941	O68941 rhodospiril
34	4	11.8	36	4	Q8WXW8	Q8wxw8 homo sapien
35	4	11.8	36	10	Q9SJ63	Q9sj63 arabidopsis
36	4	11.8	36	12	Q9PXD1	Q9pxd1 hepatitis c
37	4	11.8	36	12	Q91D77	Q91d77 ttv-like mi
38	4	11.8	36	13	Q9YHT9	Q9yht9 brachydanio
39	4	11.8	36	16	Q97S91	Q97s91 streptococc
40	4	11.8	37	2	Q8KYJ0	Q8kyj0 bacillus an
41	4	11.8	37	5	Q9N2L2	Q9n2l2 caenorhabdi
42	4	11.8	37	10	Q39942	Q39942 helianthus
43	4	11.8	37	13	Q8AWW8	Q8aww8 oncorhynch
44	4	11.8	37	16	Q8F6U2	Q8f6u2 leptospira
45	4	11.8	37	16	Q8F5H3	Q8f5h3 leptospira
46	4	11.8	37	16	Q8F419	Q8f419 leptospira
47	4	11.8	37	16	Q8EXV9	Q8exv9 leptospira
48	4	11.8	38	2	Q8KWH7	Q8kwh7 lactobacill
49	4	11.8	38	5	Q9NBE3	Q9nbe3 chironomus
50	4	11.8	38	5	Q9NBE5	Q9nbe5 chironomus
51	4	11.8	38	5	Q9NBE8	Q9nbe8 chironomus
52	4	11.8	38	5	Q9NBE4	Q9nbe4 chironomus
53	4	11.8	38	5	Q9NBE7	Q9nbe7 chironomus
54	4	11.8	38	11	Q91VC8	Q91vc8 mus musculu
55	4	11.8	38	13	Q8AWW9	Q8aww9 oncorhynch
56	4	11.8	38	16	Q8E0D2	Q8e0d2 streptococc
57	4	11.8	39	2	Q8GPPQ8	Q8gppq8 pseudomonas

58	4	11.8	39	4	Q9HAS7	Q9has7 homo sapien
59	4	11.8	39	4	Q8NG13	Q8ng13 homo sapien
60	4	11.8	39	12	Q68847	Q68847 hepatitis c
61	4	11.8	39	12	Q68845	Q68845 hepatitis c
62	4	11.8	39	12	Q68846	Q68846 hepatitis c
63	4	11.8	39	13	Q90776	Q90776 gallus gall
64	4	11.8	39	16	Q9KYH4	Q9kyh4 streptomyce
65	4	11.8	39	16	Q8F0C7	Q8f0c7 leptospira
66	4	11.8	40	2	Q8GCS7	Q8gcs7 eubacterium
67	4	11.8	40	6	Q29283	Q29283 sus scrofa
68	4	11.8	40	12	Q91JZ7	Q91jz7 hepatitis c
69	3	8.8	28	2	Q01303	Q01303 treponema p
70	3	8.8	28	2	Q05574	Q05574 prochloroth
71	3	8.8	28	2	Q9ZB83	Q9zb83 vibrio angu
72	3	8.8	28	3	Q8TGT8	Q8tgt8 saccharomyc
73	3	8.8	28	4	Q96SD9	Q96sd9 homo sapien
74	3	8.8	28	4	Q16326	Q16326 homo sapien
75	3	8.8	28	4	Q8WUY6	Q8wuy6 homo sapien
76	3	8.8	28	4	Q8NG21	Q8ng21 homo sapien
77	3	8.8	28	4	Q96EU0	Q96eu0 homo sapien
78	3	8.8	28	4	O75980	O75980 homo sapien
79	3	8.8	28	4	O95737	O95737 homo sapien
80	3	8.8	28	5	Q95P93	Q95p93 mesobuthus
81	3	8.8	28	5	Q8MUW0	Q8muw0 schistosoma
82	3	8.8	28	5	Q8MPY2	Q8mpy2 caenorhabdi
83	3	8.8	28	5	Q9BJE4	Q9bje4 pauropus sp
84	3	8.8	28	6	O62821	O62821 bubalus bub
85	3	8.8	28	6	Q9XS89	Q9xs89 equus cabal
86	3	8.8	28	8	Q8WBC8	Q8wbc8 cucurbita e
87	3	8.8	28	8	Q9TIE9	Q9tie9 centella er
88	3	8.8	28	8	Q9TIE8	Q9tie8 centella as
89	3	8.8	28	8	Q9MR96	Q9mr96 crocodylus
90	3	8.8	28	8	Q9TIE6	Q9tie6 centella hi
91	3	8.8	28	8	Q9ZYS4	Q9zys4 leishmania
92	3	8.8	28	8	Q9MR94	Q9mr94 chelonia my
93	3	8.8	28	8	Q9TIE7	Q9tie7 centella tr
94	3	8.8	28	8	Q8HS23	Q8hs23 pisum sativ
95	3	8.8	28	8	Q8HS11	Q8hs11 spathiphyll
96	3	8.8	28	8	Q8HS07	Q8hs07 welwitschia
97	3	8.8	28	8	Q8HKF0	Q8hkf0 rhipicephal
98	3	8.8	28	9	Q9AZJ9	Q9azj9 bacterioph
99	3	8.8	28	9	Q38269	Q38269 bacterioph
100	3	8.8	28	10	Q8S526	Q8s526 ipomoea bat
101	3	8.8	28	10	Q9XGH2	Q9xgh2 pisum sativ
102	3	8.8	28	10	Q9XGE3	Q9xge3 vicia faba
103	3	8.8	28	10	Q8W232	Q8w232 zea mays (m
104	3	8.8	28	10	Q9LMD6	Q9lmd6 arabidopsis
105	3	8.8	28	10	Q9XGH4	Q9xgh4 pisum sativ
106	3	8.8	28	10	Q9XGE4	Q9xge4 vicia faba
107	3	8.8	28	10	Q8GZQ8	Q8gzzq8 hordeum vul
108	3	8.8	28	11	Q9ESI4	Q9esi4 petromus ty
109	3	8.8	28	11	Q9ESI5	Q9esi5 thryonomys
110	3	8.8	28	11	Q9ESI6	Q9esi6 hystrix afr
111	3	8.8	28	11	Q99PL9	Q99pl9 mus musculu
112	3	8.8	28	11	Q9ESI2	Q9esi2 cryptomys h
113	3	8.8	28	11	Q64681	Q64681 mesocricetu
114	3	8.8	28	11	Q9EP60	Q9ep60 heliophobi

115	3	8.8	28	11	Q9ESI0	Q9esi0 cryptomys s
116	3	8.8	28	11	Q91XP0	Q91xp0 rattus norv
117	3	8.8	28	11	P70651	P70651 mus sp. bet
118	3	8.8	28	11	Q9EP59	Q9ep59 georychus c
119	3	8.8	28	11	Q9ESI1	Q9esi1 cryptomys d
120	3	8.8	28	11	P97914	P97914 rattus norv
121	3	8.8	28	11	Q9EP61	Q9ep61 heteroceph
122	3	8.8	28	11	Q9ESH8	Q9esh8 bathyergus
123	3	8.8	28	11	Q9ESH9	Q9esh9 bathyergus
124	3	8.8	28	11	Q9QXB4	Q9qxb4 mus musculu
125	3	8.8	28	11	Q9ESI3	Q9esi3 cryptomys h
126	3	8.8	28	12	Q68087	Q68087 hepatitis c
127	3	8.8	28	12	Q67786	Q67786 human adeno
128	3	8.8	28	12	Q68095	Q68095 hepatitis c
129	3	8.8	28	12	Q68097	Q68097 hepatitis c
130	3	8.8	28	12	Q68092	Q68092 hepatitis c
131	3	8.8	28	12	Q68091	Q68091 hepatitis c
132	3	8.8	28	12	Q68093	Q68093 hepatitis c
133	3	8.8	28	12	Q68099	Q68099 hepatitis c
134	3	8.8	28	12	Q68096	Q68096 hepatitis c
135	3	8.8	28	12	Q68098	Q68098 hepatitis c
136	3	8.8	28	12	Q83181	Q83181 cauliflower
137	3	8.8	28	12	Q68086	Q68086 hepatitis c
138	3	8.8	28	12	Q68552	Q68552 hepatitis c
139	3	8.8	28	12	Q68094	Q68094 hepatitis c
140	3	8.8	28	12	Q9WNI4	Q9wni4 tt virus. o
141	3	8.8	28	13	Q9PRE8	Q9pre8 oryzias lat
142	3	8.8	28	13	Q9PRI9	Q9pri9 amia calva
143	3	8.8	28	13	Q9PRN8	Q9prn8 carassius a
144	3	8.8	28	15	O71346	O71346 human endog
145	3	8.8	28	15	Q9QEY3	Q9qey3 human immun
146	3	8.8	28	16	Q8X415	Q8x415 escherichia
147	3	8.8	28	16	Q8NVB8	Q8nvb8 staphylococ
148	3	8.8	28	16	Q8ENT7	Q8ent7 oceanobacil
149	3	8.8	28	16	Q8CK95	Q8ck95 yersinia pe
150	3	8.8	29	2	Q9ZGG4	Q9zgg4 heliobacill
151	3	8.8	29	2	Q48358	Q48358 escherichia
152	3	8.8	29	2	Q54200	Q54200 streptomyce
153	3	8.8	29	2	Q9X3E3	Q9x3e3 prochloroco
154	3	8.8	29	2	Q9X3J9	Q9x3j9 prochloroco
155	3	8.8	29	2	Q9Z4G6	Q9z4g6 salmonella
156	3	8.8	29	2	Q47650	Q47650 escherichia
157	3	8.8	29	2	Q9AKV1	Q9akv1 neisseria g
158	3	8.8	29	3	P78747	P78747 saccharomyc
159	3	8.8	29	3	Q8TGQ5	Q8tgg5 saccharomyc
160	3	8.8	29	4	Q9Y3G1	Q9y3g1 homo sapien
161	3	8.8	29	4	Q9H2A1	Q9h2a1 homo sapien
162	3	8.8	29	4	Q9UN87	Q9un87 homo sapien
163	3	8.8	29	4	Q9H465	Q9h465 homo sapien
164	3	8.8	29	4	Q8NEF6	Q8nef6 homo sapien
165	3	8.8	29	4	Q8TDW8	Q8tdw8 homo sapien
166	3	8.8	29	4	Q96IR5	Q96ir5 homo sapien
167	3	8.8	29	4	Q9BSQ3	Q9bsq3 homo sapien
168	3	8.8	29	5	Q95VB2	Q95vb2 spirometra
169	3	8.8	29	5	Q95NF4	Q95nf4 drosophila
170	3	8.8	29	5	Q24683	Q24683 dugesia tig
171	3	8.8	29	6	Q9TRG5	Q9trg5 sus scrofa

172	3	8.8	29	8	Q8WBB9	Q8wbb9	cucurbita f
173	3	8.8	29	8	Q9TI57	Q9ti57	corymbia pa
174	3	8.8	29	8	Q8W7W7	Q8w7w7	cucurbita p
175	3	8.8	29	8	Q9GF70	Q9gf70	trochodendr
176	3	8.8	29	8	Q8W7W4	Q8w7w4	cucurbita a
177	3	8.8	29	8	Q8W7W6	Q8w7w6	cucurbita p
178	3	8.8	29	8	Q8WBC1	Q8wbc1	cucurbita o
179	3	8.8	29	8	Q9B5Z6	Q9b5z6	pseudostylo
180	3	8.8	29	8	Q8W7W5	Q8w7w5	cucurbita p
181	3	8.8	29	8	Q9B938	Q9b938	eupristina
182	3	8.8	29	8	Q9G370	Q9g370	draco blanf
183	3	8.8	29	8	Q8WBD0	Q8wbd0	cucurbita a
184	3	8.8	29	8	Q8WBB6	Q8wbb6	citrullus l
185	3	8.8	29	8	Q8W7W9	Q8w7w9	cucurbita f
186	3	8.8	29	8	Q8W7W8	Q8w7w8	cucurbita m
187	3	8.8	29	8	Q8HS21	Q8hs21	rheum x cul
188	3	8.8	29	9	Q9FZX6	Q9fzx6	bacterioph
189	3	8.8	29	10	P82196	P82196	spinacia ol
190	3	8.8	29	11	Q9Z2C0	Q9z2c0	mus musculu
191	3	8.8	29	11	Q921Z6	Q921z6	mus musculu
192	3	8.8	29	11	Q9Z2C1	Q9z2c1	mus musculu
193	3	8.8	29	11	070564	070564	mus musculu
194	3	8.8	29	11	Q9QY65	Q9qy65	mus musculu
195	3	8.8	29	11	Q62300	Q62300	mus musculu
196	3	8.8	29	11	008980	008980	mus musculu
197	3	8.8	29	11	Q8CGM8	Q8cgm8	mus musculu
198	3	8.8	29	12	Q91HB1	Q91hb1	porcine cir
199	3	8.8	29	12	092646	092646	hepatitis e
200	3	8.8	29	12	Q919A5	Q919a5	porcine rep
201	3	8.8	29	12	Q919A7	Q919a7	porcine rep
202	3	8.8	29	12	Q86872	Q86872	cauliflower
203	3	8.8	29	12	092648	092648	hepatitis e
204	3	8.8	29	12	056835	056835	vibrio chol
205	3	8.8	29	13	Q8AYR0	Q8ayr0	oryzias lat
206	3	8.8	29	13	Q8AWC2	Q8awc2	gallus gall
207	3	8.8	29	15	072001	072001	human endog
208	3	8.8	29	15	071342	071342	human endog
209	3	8.8	29	15	071339	071339	human endog
210	3	8.8	29	15	071347	071347	human endog
211	3	8.8	29	15	071340	071340	human endog
212	3	8.8	29	15	071343	071343	human endog
213	3	8.8	29	15	Q9IQJ8	Q9iqj8	human immun
214	3	8.8	29	15	071991	071991	human endog
215	3	8.8	29	15	Q9Q3C7	Q9q3c7	human immun
216	3	8.8	29	15	Q9IQJ1	Q9iqj1	human immun
217	3	8.8	29	15	071994	071994	human endog
218	3	8.8	29	15	071341	071341	human endog
219	3	8.8	29	15	071345	071345	human endog
220	3	8.8	29	15	071336	071336	human endog
221	3	8.8	29	15	071344	071344	human endog
222	3	8.8	29	15	071338	071338	human endog
223	3	8.8	29	15	071992	071992	human endog
224	3	8.8	29	15	071337	071337	human endog
225	3	8.8	29	15	Q9IQJ9	Q9iqj9	human immun
226	3	8.8	29	15	071997	071997	human endog
227	3	8.8	29	15	071335	071335	human endog
228	3	8.8	29	16	Q8X419	Q8x419	escherichia

229	3	8.8	29	17	Q8Q0H5	Q8q0h5 methanosarc
230	3	8.8	30	2	Q9JP75	Q9jp75 salmonella
231	3	8.8	30	2	Q9L8W9	Q9l8w9 streptomyce
232	3	8.8	30	2	Q9L8X1	Q9l8x1 streptomyce
233	3	8.8	30	2	Q9R4Z6	Q9r4z6 clostridium
234	3	8.8	30	2	Q9REI5	Q9rei5 acidiphiliu
235	3	8.8	30	2	Q9R4J2	Q9r4j2 helicobacte
236	3	8.8	30	2	Q8VUW9	Q8vuw9 staphylococ
237	3	8.8	30	2	Q9R4I5	Q9r4i5 mycoplasma
238	3	8.8	30	2	Q9R5Q3	Q9r5q3 leuconostoc
239	3	8.8	30	2	Q45966	Q45966 coxiella bu
240	3	8.8	30	2	Q9R5C4	Q9r5c4 comamonas.
241	3	8.8	30	2	Q9R4I6	Q9r4i6 mycoplasma
242	3	8.8	30	2	Q9RER6	Q9rer6 enterobacte
243	3	8.8	30	3	Q9URB0	Q9urb0 candida alb
244	3	8.8	30	3	Q8J172	Q8j172 trichoderma
245	3	8.8	30	3	Q8J171	Q8j171 hypocrea li
246	3	8.8	30	4	Q16330	Q16330 homo sapien
247	3	8.8	30	4	O95595	O95595 homo sapien
248	3	8.8	30	4	P78460	P78460 homo sapien
249	3	8.8	30	4	Q8N563	Q8n563 homo sapien
250	3	8.8	30	4	P78542	P78542 homo sapien
251	3	8.8	30	5	Q9TWH7	Q9twh7 ancylostoma
252	3	8.8	30	5	Q968N1	Q968n1 tritrichomo
253	3	8.8	30	5	P82214	P82214 bombyx mori
254	3	8.8	30	6	Q9BDK1	Q9bdk1 bos taurus
255	3	8.8	30	6	Q28227	Q28227 dama dama (
256	3	8.8	30	6	Q29431	Q29431 ovis aries
257	3	8.8	30	6	Q27997	Q27997 bos taurus
258	3	8.8	30	6	Q9TTF9	Q9ttf9 ateles belz
259	3	8.8	30	8	Q8W7L1	Q8w7l1 cucurbita m
260	3	8.8	30	8	Q8W7K9	Q8w7k9 cucurbita p
261	3	8.8	30	8	Q8W7H8	Q8w7h8 cucurbita a
262	3	8.8	30	8	Q8WBC2	Q8wbc2 cucurbita o
263	3	8.8	30	8	Q8W7K8	Q8w7k8 cucurbita p
264	3	8.8	30	8	Q8W7H6	Q8w7h6 cucurbita m
265	3	8.8	30	8	Q8WBC4	Q8wbc4 cucurbita p
266	3	8.8	30	8	Q8W7L2	Q8w7l2 cucurbita a
267	3	8.8	30	8	Q8WBC6	Q8wbc6 cucurbita a
268	3	8.8	30	8	Q8WBB7	Q8wbb7 sechium edu
269	3	8.8	30	8	Q99328	Q99328 meloidogyne
270	3	8.8	30	8	Q8W7H7	Q8w7h7 cucurbita e
271	3	8.8	30	8	Q8WBC0	Q8wbc0 cucurbita f
272	3	8.8	30	8	Q8W7L0	Q8w7l0 cucurbita p
273	3	8.8	30	8	Q9TI56	Q9ti56 eucalyptus
274	3	8.8	30	8	Q8HKG1	Q8hkg1 rhipicephal
275	3	8.8	30	9	Q8W674	Q8w674 enterobacte
276	3	8.8	30	10	Q9S8T2	Q9s8t2 cicer ariet
277	3	8.8	30	10	O23933	O23933 flaveria tr
278	3	8.8	30	10	Q8RUD1	Q8rud1 zea mays (m
279	3	8.8	30	10	Q93WY2	Q93wy2 oryza sativ
280	3	8.8	30	11	Q63885	Q63885 mus sp. cys
281	3	8.8	30	11	O88549	O88549 mesocricetu
282	3	8.8	30	11	Q8VDL1	Q8vdl1 mus musculu
283	3	8.8	30	11	Q9QV14	Q9qv14 mus sp. col
284	3	8.8	30	11	Q10753	Q10753 rattus norv
285	3	8.8	30	11	Q8BR32	Q8br32 mus musculu

286	3	8.8	30	12	Q91HB7	Q91hb7	tt virus. o
287	3	8.8	30	12	Q91HC4	Q91hc4	tt virus. o
288	3	8.8	30	12	Q9IJV5	Q9ijv5	norwalk vir
289	3	8.8	30	12	Q86870	Q86870	cauliflower
290	3	8.8	30	12	Q91HC3	Q91hc3	tt virus. o
291	3	8.8	30	12	Q9WLK3	Q9wlk3	hepatitis e
292	3	8.8	30	12	Q91HC0	Q91hc0	tt virus. o
293	3	8.8	30	13	O42551	O42551	brachydanio
294	3	8.8	30	13	Q9PRW0	Q9prw0	struthio ca
295	3	8.8	30	13	Q9PT00	Q9pt00	oncorhynchu
296	3	8.8	30	15	Q86599	Q86599	human endog
297	3	8.8	30	15	Q991P5	Q991p5	human immun
298	3	8.8	30	16	O50822	O50822	borrelia bu
299	3	8.8	30	16	Q9X0W9	Q9x0w9	thermotoga
300	3	8.8	30	16	Q9PP53	Q9pp53	campylobact
301	3	8.8	30	16	Q9KU55	Q9ku55	vibrio chol
302	3	8.8	30	16	Q9KT75	Q9kt75	vibrio chol
303	3	8.8	30	16	Q9AC21	Q9ac21	caulobacter
304	3	8.8	30	16	Q97SY9	Q97sy9	streptococc
305	3	8.8	30	16	Q97SX5	Q97sx5	streptococc
306	3	8.8	30	16	Q9K1W7	Q9klw7	chlamydia p
307	3	8.8	30	16	Q8U566	Q8u566	agrobacteri
308	3	8.8	30	16	Q8KE55	Q8ke55	chlorobium
309	3	8.8	30	16	Q8G1R1	Q8glr1	brucella su
310	3	8.8	30	16	Q8FZX9	Q8fzx9	brucella su
311	3	8.8	30	16	Q8CU88	Q8cu88	staphylococ
312	3	8.8	30	17	Q8ZZF0	Q8zzf0	pyrobaculum
313	3	8.8	30	17	Q8ZVL0	Q8zvl0	pyrobaculum
314	3	8.8	31	2	Q45547	Q45547	bacillus su
315	3	8.8	31	2	Q9S619	Q9s619	prochloroco
316	3	8.8	31	2	Q8KYK0	Q8kyk0	bacillus an
317	3	8.8	31	2	Q9JMV2	Q9jmv2	escherichia
318	3	8.8	31	2	Q9X3C3	Q9x3c3	prochloroco
319	3	8.8	31	2	O68825	O68825	pseudomonas
320	3	8.8	31	2	Q9KH08	Q9kh08	thermus aqu
321	3	8.8	31	2	Q47323	Q47323	escherichia
322	3	8.8	31	2	Q9RHF9	Q9rhf9	acinetobact
323	3	8.8	31	2	Q8KYI9	Q8kyi9	bacillus an
324	3	8.8	31	2	Q8RTS5	Q8rts5	uncultured
325	3	8.8	31	2	Q8L3D3	Q8l3d3	colwellia m
326	3	8.8	31	2	Q93PE1	Q93pe1	yersinia ps
327	3	8.8	31	3	O94120	O94120	saccharomyc
328	3	8.8	31	3	Q9USG3	Q9usg3	schizosacch
329	3	8.8	31	4	Q96A45	Q96a45	homo sapien
330	3	8.8	31	4	Q9UEA9	Q9uea9	homo sapien
331	3	8.8	31	4	Q8WYF5	Q8wyf5	homo sapien
332	3	8.8	31	4	Q8N5X3	Q8n5x3	homo sapien
333	3	8.8	31	4	Q9BXM4	Q9bxm4	homo sapien
334	3	8.8	31	4	Q9UDE5	Q9ude5	homo sapien
335	3	8.8	31	5	Q8IQV3	Q8iqv3	drosophila
336	3	8.8	31	5	Q8IEY3	Q8iey3	trypanosoma
337	3	8.8	31	6	Q9GLD6	Q9gld6	sus scrofa
338	3	8.8	31	6	Q8MIH5	Q8mih5	canis famil
339	3	8.8	31	6	O77625	O77625	bos taurus
340	3	8.8	31	6	Q95LC0	Q95lc0	sus scrofa
341	3	8.8	31	6	Q9N1C8	Q9n1c8	ovis aries
342	3	8.8	31	6	Q9XSB9	Q9xsb9	ateles belz

343	3	8.8	31	7	Q29868	Q29868	homo sapien
344	3	8.8	31	8	Q9MNM2	Q9mnm2	bufo americ
345	3	8.8	31	8	O80011	O80011	enallagma a
346	3	8.8	31	8	Q34922	Q34922	limulus pol
347	3	8.8	31	8	Q8WEJ4	Q8wej4	gnetum gnem
348	3	8.8	31	8	Q8M9Y3	Q8m9y3	chaetosphae
349	3	8.8	31	8	Q9MNL2	Q9mnl2	torrentophr
350	3	8.8	31	8	Q9MS78	Q9ms78	phacus acum
351	3	8.8	31	8	Q9MNL3	Q9mnl3	torrentophr
352	3	8.8	31	9	Q38499	Q38499	bacteriopha
353	3	8.8	31	10	Q9XIT0	Q9xit0	glycine max
354	3	8.8	31	11	Q9QXB6	Q9qxb6	mus musculu
355	3	8.8	31	11	Q99KK6	Q99kk6	mus musculu
356	3	8.8	31	11	O55182	O55182	rattus norv
357	3	8.8	31	11	Q8CGM7	Q8cgm7	mus musculu
358	3	8.8	31	12	Q919E5	Q919e5	human papil
359	3	8.8	31	12	Q919E4	Q919e4	human papil
360	3	8.8	31	12	O56713	O56713	hepatitis c
361	3	8.8	31	12	Q919F7	Q919f7	human papil
362	3	8.8	31	12	Q919E6	Q919e6	human papil
363	3	8.8	31	12	O56692	O56692	hepatitis c
364	3	8.8	31	12	Q919F3	Q919f3	human papil
365	3	8.8	31	12	O56707	O56707	hepatitis c
366	3	8.8	31	12	O56687	O56687	hepatitis c
367	3	8.8	31	12	Q919F8	Q919f8	human papil
368	3	8.8	31	12	O56691	O56691	hepatitis c
369	3	8.8	31	12	Q919E1	Q919e1	human papil
370	3	8.8	31	12	O56701	O56701	hepatitis c
371	3	8.8	31	12	O56694	O56694	hepatitis c
372	3	8.8	31	12	Q919D9	Q919d9	human papil
373	3	8.8	31	12	Q919F6	Q919f6	human papil
374	3	8.8	31	12	Q919E3	Q919e3	human papil
375	3	8.8	31	12	O56712	O56712	hepatitis c
376	3	8.8	31	12	Q919E8	Q919e8	human papil
377	3	8.8	31	12	O56710	O56710	hepatitis c
378	3	8.8	31	12	O56688	O56688	hepatitis c
379	3	8.8	31	12	O56696	O56696	hepatitis c
380	3	8.8	31	12	O56695	O56695	hepatitis c
381	3	8.8	31	12	O56698	O56698	hepatitis c
382	3	8.8	31	12	O56702	O56702	hepatitis c
383	3	8.8	31	12	O56703	O56703	hepatitis c
384	3	8.8	31	12	O56697	O56697	hepatitis c
385	3	8.8	31	12	Q919F0	Q919f0	human papil
386	3	8.8	31	12	O56709	O56709	hepatitis c
387	3	8.8	31	12	Q919F4	Q919f4	human papil
388	3	8.8	31	12	O56689	O56689	hepatitis c
389	3	8.8	31	12	Q919F2	Q919f2	human papil
390	3	8.8	31	12	Q919F1	Q919f1	human papil
391	3	8.8	31	12	Q86568	Q86568	hepatitis d
392	3	8.8	31	12	O56711	O56711	hepatitis c
393	3	8.8	31	12	Q84108	Q84108	influenza v
394	3	8.8	31	12	Q919E2	Q919e2	human papil
395	3	8.8	31	12	Q919D8	Q919d8	human papil
396	3	8.8	31	12	O56686	O56686	hepatitis c
397	3	8.8	31	12	Q9WMX5	Q9wmx5	human echov
398	3	8.8	31	12	O56690	O56690	hepatitis c
399	3	8.8	31	12	Q919E9	Q919e9	human papil

400	3	8.8	31	12	056706	056706 hepatitis c
401	3	8.8	31	12	056700	056700 hepatitis c
402	3	8.8	31	12	056704	056704 hepatitis c
403	3	8.8	31	12	Q919D7	Q919d7 human papil
404	3	8.8	31	12	Q919F5	Q919f5 human papil
405	3	8.8	31	12	056693	056693 hepatitis c
406	3	8.8	31	12	056685	056685 hepatitis c
407	3	8.8	31	12	056708	056708 hepatitis c
408	3	8.8	31	12	Q919E0	Q919e0 human papil
409	3	8.8	31	12	056705	056705 hepatitis c
410	3	8.8	31	12	Q919E7	Q919e7 human papil
411	3	8.8	31	12	Q914M9	Q914m9 sulfolobus
412	3	8.8	31	12	056699	056699 hepatitis c
413	3	8.8	31	13	042540	042540 brachydanio
414	3	8.8	31	13	Q91763	Q91763 xenopus lae
415	3	8.8	31	13	Q9PSU1	Q9psu1 xenopus lae
416	3	8.8	31	13	Q91816	Q91816 xenopus lae
417	3	8.8	31	16	050709	050709 borrelia bu
418	3	8.8	31	16	050818	050818 borrelia bu
419	3	8.8	31	16	050858	050858 borrelia bu
420	3	8.8	31	16	051007	051007 borrelia bu
421	3	8.8	31	16	Q9PGF2	Q9pgf2 xylella fas
422	3	8.8	31	16	Q9PAW4	Q9paw4 xylella fas
423	3	8.8	31	16	Q9KVF3	Q9kvf3 vibrio chol
424	3	8.8	31	16	Q9K7A8	Q9k7a8 bacillus ha
425	3	8.8	31	16	Q9AAD8	Q9aad8 caulobacter
426	3	8.8	31	16	Q97SZ9	Q97sz9 streptococc
427	3	8.8	31	16	Q97SW8	Q97sw8 streptococc
428	3	8.8	31	16	Q97QB7	Q97qb7 streptococc
429	3	8.8	31	16	Q97CV6	Q97cv6 streptococc
430	3	8.8	31	16	Q9K2A0	Q9k2a0 chlamydia p
431	3	8.8	31	16	Q9K236	Q9k236 chlamydia p
432	3	8.8	31	16	Q8P9W1	Q8p9w1 xanthomonas
433	3	8.8	31	16	Q8KEV8	Q8kev8 chlorobium
434	3	8.8	31	16	Q8KCQ0	Q8kcq0 chlorobium
435	3	8.8	31	16	Q8KBJ8	Q8kbj8 chlorobium
436	3	8.8	31	16	Q8G1E2	Q8gle2 brucella su
437	3	8.8	31	16	Q8EIW8	Q8eiw8 shewanella
438	3	8.8	31	16	Q8EI77	Q8ei77 shewanella
439	3	8.8	31	16	Q8E9Y5	Q8e9y5 shewanella
440	3	8.8	31	16	Q8E8G1	Q8e8g1 shewanella
441	3	8.8	31	16	Q8CTW3	Q8ctw3 staphylococ
442	3	8.8	31	16	Q8CTA2	Q8cta2 staphylococ
443	3	8.8	32	2	Q9AJ41	Q9aj41 buchnera ap
444	3	8.8	32	2	Q00491	Q00491 streptomyce
445	3	8.8	32	2	Q49249	Q49249 mycoplasma
446	3	8.8	32	2	Q44499	Q44499 anabaena va
447	3	8.8	32	2	Q9S629	Q9s629 prochloroco
448	3	8.8	32	2	Q8KYN3	Q8kyn3 bacillus an
449	3	8.8	32	2	Q44509	Q44509 azotobacter
450	3	8.8	32	2	Q45534	Q45534 bacillus su
451	3	8.8	32	2	Q8VN21	Q8vn21 kluyvera ci
452	3	8.8	32	2	Q9R5Q7	Q9r5q7 aeromonas h
453	3	8.8	32	2	Q8KYM4	Q8kym4 bacillus an
454	3	8.8	32	2	O32493	O32493 bacteroides
455	3	8.8	32	2	Q8VNT6	Q8vnt6 enterobacte
456	3	8.8	32	2	Q9L373	Q9l373 rhizobium l

457	3	8.8	32	2	Q8GF58	Q8gf58	zymomonas m
458	3	8.8	32	3	Q01058	Q01058	kluyveromyc
459	3	8.8	32	3	Q8TGT3	Q8tgt3	saccharomyc
460	3	8.8	32	4	Q12900	Q12900	homo sapien
461	3	8.8	32	4	Q9UEB0	Q9ueb0	homo sapien
462	3	8.8	32	4	Q8TC25	Q8tc25	homo sapien
463	3	8.8	32	4	Q96GM7	Q96gm7	homo sapien
464	3	8.8	32	4	Q8TBQ3	Q8tbq3	homo sapien
465	3	8.8	32	4	Q96I20	Q96i20	homo sapien
466	3	8.8	32	4	Q9UN69	Q9un69	homo sapien
467	3	8.8	32	4	Q9UQV1	Q9uqv1	homo sapien
468	3	8.8	32	5	Q9GPD9	Q9gpd9	drosophila
469	3	8.8	32	5	Q8T382	Q8t382	leishmania
470	3	8.8	32	5	O96634	O96634	trypanosoma
471	3	8.8	32	5	Q9TWR8	Q9twr8	procambarus
472	3	8.8	32	5	O18606	O18606	branchiosto
473	3	8.8	32	5	Q8T757	Q8t757	branchiosto
474	3	8.8	32	6	Q9TR67	Q9tr67	sus scrofa
475	3	8.8	32	6	Q9TR69	Q9tr69	sus scrofa
476	3	8.8	32	6	Q9TSE6	Q9tse6	oryctolagus
477	3	8.8	32	6	Q8MJ91	Q8mj91	macaca mula
478	3	8.8	32	6	Q9N1V7	Q9nlv7	equus cabal
479	3	8.8	32	6	O77647	O77647	macropus eu
480	3	8.8	32	6	Q8I035	Q8i035	sus scrofa
481	3	8.8	32	7	Q8SNF1	Q8snf1	gallinago m
482	3	8.8	32	7	O19722	O19722	homo sapien
483	3	8.8	32	8	Q36494	Q36494	farfantepen
484	3	8.8	32	8	Q8SL89	Q8sl89	euglena ste
485	3	8.8	32	8	Q9GF95	Q9gf95	cercidiphyl
486	3	8.8	32	8	Q31736	Q31736	beta vulgar
487	3	8.8	32	8	Q8SL87	Q8sl87	euglena vir
488	3	8.8	32	8	Q31735	Q31735	beta vulgar
489	3	8.8	32	8	Q9MNM0	Q9mnm0	bufo andrew
490	3	8.8	32	8	Q9MNL0	Q9mnl0	bufo danate
491	3	8.8	32	8	Q951Q4	Q951q4	renilla ren
492	3	8.8	32	8	Q9GF72	Q9gf72	saururus ce
493	3	8.8	32	9	Q9MBU5	Q9mbu5	chlamydia p
494	3	8.8	32	10	Q8S527	Q8s527	ipomoea bat
495	3	8.8	32	10	Q8RXQ5	Q8rxq5	arabidopsis
496	3	8.8	32	10	Q40727	Q40727	oryza sativ
497	3	8.8	32	11	Q9JIU1	Q9jiu1	rattus norv
498	3	8.8	32	11	Q9R0E3	Q9r0e3	mus musculu
499	3	8.8	32	11	Q9QWM2	Q9qwm2	mus musculu
500	3	8.8	32	11	Q9QWB2	Q9qwb2	rattus sp.
501	3	8.8	32	11	Q9QXX1	Q9qxx1	mus musculu
502	3	8.8	32	11	Q8C2N8	Q8c2n8	mus musculu
503	3	8.8	32	12	Q9PXV2	Q9pxv2	hepatitis b
504	3	8.8	32	12	Q9WNI5	Q9wni5	tt virus. o
505	3	8.8	32	12	Q914F9	Q914f9	sulfolobus
506	3	8.8	32	12	Q8QYT4	Q8qyt4	grapevine v
507	3	8.8	32	12	Q8QYT7	Q8qyt7	grapevine v
508	3	8.8	32	12	Q8QYU0	Q8qyu0	grapevine v
509	3	8.8	32	12	Q9Q934	Q9q934	shope fibro
510	3	8.8	32	13	Q8QG73	Q8qg73	oncorhynchu
511	3	8.8	32	13	Q8QG72	Q8qg72	salmo salar
512	3	8.8	32	13	Q8QG71	Q8qg71	oncorhynchu
513	3	8.8	32	13	Q9PS21	Q9ps21	carassius a

514	3	8.8	32	13	Q8QG84	Q8qg84	oncorhynchu
515	3	8.8	32	13	Q8QG83	Q8qg83	oncorhynchu
516	3	8.8	32	13	Q8QG82	Q8qg82	oncorhynchu
517	3	8.8	32	13	Q8QG70	Q8qg70	salvelinus
518	3	8.8	32	16	O50706	O50706	borrelia bu
519	3	8.8	32	16	O50851	O50851	borrelia bu
520	3	8.8	32	16	O50865	O50865	borrelia bu
521	3	8.8	32	16	O51003	O51003	borrelia bu
522	3	8.8	32	16	Q9PGT0	Q9pgt0	xylella fas
523	3	8.8	32	16	Q9KVF7	Q9kvf7	vibrio chol
524	3	8.8	32	16	Q9KTV2	Q9ktv2	vibrio chol
525	3	8.8	32	16	Q9KPN9	Q9kpn9	vibrio chol
526	3	8.8	32	16	Q9KLF0	Q9klf0	vibrio chol
527	3	8.8	32	16	Q9K7B0	Q9k7b0	bacillus ha
528	3	8.8	32	16	Q9K175	Q9k175	neisseria m
529	3	8.8	32	16	Q9A2H0	Q9a2h0	caulobacter
530	3	8.8	32	16	Q98AB6	Q98ab6	rhizobium l
531	3	8.8	32	16	Q8X3V6	Q8x3v6	escherichia
532	3	8.8	32	16	Q8PEL7	Q8pel7	xanthomonas
533	3	8.8	32	16	Q8KG49	Q8kg49	chlorobium
534	3	8.8	32	16	Q8KEZ9	Q8kez9	chlorobium
535	3	8.8	32	16	Q8KE29	Q8ke29	chlorobium
536	3	8.8	32	16	Q8KCV3	Q8kcv3	chlorobium
537	3	8.8	32	16	Q8KCP1	Q8kcp1	chlorobium
538	3	8.8	32	16	Q9K4G0	Q9k4g0	streptomyce
539	3	8.8	32	16	Q8EJ44	Q8ej44	shewanella
540	3	8.8	32	16	Q8EAD5	Q8ead5	shewanella
541	3	8.8	32	16	Q8CU60	Q8cu60	staphylococ
542	3	8.8	32	16	Q8CTR7	Q8ctr7	staphylococ
543	3	8.8	32	16	Q8CRE7	Q8cre7	staphylococ
544	3	8.8	32	17	Q8ZZF7	Q8zzf7	pyrobaculum
545	3	8.8	33	2	Q8KH96	Q8kh96	pseudomonas
546	3	8.8	33	2	Q9S624	Q9s624	prochloroco
547	3	8.8	33	2	Q9R2M3	Q9r2m3	prochloroco
548	3	8.8	33	2	Q9X3M5	Q9x3m5	prochloroco
549	3	8.8	33	2	Q9S651	Q9s651	streptococc
550	3	8.8	33	2	Q9K533	Q9k533	listeria mo
551	3	8.8	33	2	Q9K370	Q9k370	rhizobium l
552	3	8.8	33	2	Q9F2C4	Q9f2c4	salmonella
553	3	8.8	33	2	Q8KQ80	Q8kq80	vibrio chol
554	3	8.8	33	2	Q56414	Q56414	escherichia
555	3	8.8	33	2	Q9S622	Q9s622	prochloroco
556	3	8.8	33	2	Q9K2V1	Q9k2v1	rhizobium l
557	3	8.8	33	2	Q9F1F4	Q9f1f4	enterococcu
558	3	8.8	33	3	Q8TGR1	Q8tgr1	saccharomyc
559	3	8.8	33	4	Q99950	Q99950	homo sapien
560	3	8.8	33	4	Q8WWC1	Q8wwc1	homo sapien
561	3	8.8	33	4	Q9UP36	Q9up36	homo sapien
562	3	8.8	33	4	Q15285	Q15285	homo sapien
563	3	8.8	33	4	Q8N2V2	Q8n2v2	homo sapien
564	3	8.8	33	4	Q9UDI1	Q9udi1	homo sapien
565	3	8.8	33	4	Q92668	Q92668	homo sapien
566	3	8.8	33	5	Q9GTB2	Q9gtb2	eimeria ten
567	3	8.8	33	5	Q9GT93	Q9gt93	cryptospori
568	3	8.8	33	5	Q26673	Q26673	tethya aura
569	3	8.8	33	5	Q26672	Q26672	tethya aura
570	3	8.8	33	5	Q9GTC2	Q9gtc2	plasmodium

571	3	8.8	33	5	Q27637	Q27637 drosophila
572	3	8.8	33	5	Q9GTB3	Q9gtb3 eimeria ten
573	3	8.8	33	5	Q9GTA6	Q9gta6 sarcocystis
574	3	8.8	33	5	Q9GTA1	Q9gta1 babesia bov
575	3	8.8	33	5	Q17293	Q17293 cancer ante
576	3	8.8	33	5	Q27310	Q27310 paramecium
577	3	8.8	33	5	Q9GTA9	Q9gta9 sarcocystis
578	3	8.8	33	5	Q9GT95	Q9gt95 cryptospori
579	3	8.8	33	5	Q9GTA2	Q9gta2 babesia bov
580	3	8.8	33	5	Q9VHD7	Q9vhd7 drosophila
581	3	8.8	33	6	O18916	O18916 sus scrofa
582	3	8.8	33	6	Q9TSX7	Q9tsx7 sus scrofa
583	3	8.8	33	6	Q95M05	Q95m05 bos taurus
584	3	8.8	33	7	Q8MGU2	Q8mgu2 bos taurus
585	3	8.8	33	7	Q8SNF0	Q8snf0 gallinago m
586	3	8.8	33	8	Q9BAC6	Q9bac6 euglena gra
587	3	8.8	33	8	Q8W9G0	Q8w9g0 meloidogyne
588	3	8.8	33	8	Q9BAC1	Q9bac1 euglena ste
589	3	8.8	33	8	Q9XNP3	Q9xnp3 boophilus m
590	3	8.8	33	8	O78857	O78857 phytophthor
591	3	8.8	33	8	Q9T2N1	Q9t2n1 nicotiana t
592	3	8.8	33	8	Q9BAC4	Q9bac4 euglena mut
593	3	8.8	33	8	Q8WEJ5	Q8wej5 ginkgo bilo
594	3	8.8	33	8	Q8HUH3	Q8huh3 chlamydomon
595	3	8.8	33	8	Q8HS33	Q8hs33 hydrastis c
596	3	8.8	33	9	Q38588	Q38588 bacterioph
597	3	8.8	33	9	Q38551	Q38551 bacterioph
598	3	8.8	33	10	O49775	O49775 arabidopsis
599	3	8.8	33	10	Q9S8V5	Q9s8v5 zea mays (m
600	3	8.8	33	11	Q8BUI8	Q8bui8 mus musculu
601	3	8.8	33	12	Q90085	Q90085 human papil
602	3	8.8	33	12	Q91J04	Q91j04 tt virus. o
603	3	8.8	33	12	O72996	O72996 hepatitis c
604	3	8.8	33	12	Q91J14	Q91j14 tt virus. o
605	3	8.8	33	12	Q91J12	Q91j12 tt virus. o
606	3	8.8	33	12	Q91J15	Q91j15 tt virus. o
607	3	8.8	33	12	Q91J07	Q91j07 tt virus. o
608	3	8.8	33	12	O72995	O72995 hepatitis c
609	3	8.8	33	12	Q91J09	Q91j09 tt virus. o
610	3	8.8	33	12	Q86912	Q86912 hepatitis c
611	3	8.8	33	12	Q8V5G7	Q8v5g7 hepatitis c
612	3	8.8	33	12	Q91J08	Q91j08 tt virus. o
613	3	8.8	33	12	O72997	O72997 hepatitis c
614	3	8.8	33	12	Q83963	Q83963 avian influ
615	3	8.8	33	12	Q91J06	Q91j06 tt virus. o
616	3	8.8	33	12	O72999	O72999 hepatitis c
617	3	8.8	33	12	Q91J16	Q91j16 tt virus. o
618	3	8.8	33	12	O72998	O72998 hepatitis c
619	3	8.8	33	12	Q91J11	Q91j11 tt virus. o
620	3	8.8	33	12	O72994	O72994 hepatitis c
621	3	8.8	33	12	Q8V5H0	Q8v5h0 hepatitis c
622	3	8.8	33	12	Q91J13	Q91j13 tt virus. o
623	3	8.8	33	12	Q8V5G8	Q8v5g8 hepatitis c
624	3	8.8	33	12	O73007	O73007 hepatitis c
625	3	8.8	33	12	Q91J10	Q91j10 tt virus. o
626	3	8.8	33	12	Q91J17	Q91j17 tt virus. o
627	3	8.8	33	12	Q69461	Q69461 human herpe

628	3	8.8	33	12	Q8V5G9	Q8v5g9 hepatitis c
629	3	8.8	33	12	O73004	O73004 hepatitis c
630	3	8.8	33	12	Q99138	Q99138 avian influ
631	3	8.8	33	13	P82740	P82740 rana tempor
632	3	8.8	33	13	P82236	P82236 rana tempor
633	3	8.8	33	15	Q86107	Q86107 simian sarc
634	3	8.8	33	16	Q9PA23	Q9pa23 xylella fas
635	3	8.8	33	16	Q9KML1	Q9kml1 vibrio chol
636	3	8.8	33	16	Q97T91	Q97t91 streptococc
637	3	8.8	33	16	Q97PC1	Q97pc1 streptococc
638	3	8.8	33	16	Q932N2	Q932n2 staphylococ
639	3	8.8	33	16	Q8ZKL2	Q8zk12 salmonella
640	3	8.8	33	16	Q8Z1V4	Q8z1v4 salmonella
641	3	8.8	33	16	Q8XAJ9	Q8xaj9 escherichia
642	3	8.8	33	16	Q8U5M4	Q8u5m4 agrobacteri
643	3	8.8	33	16	Q8NUL1	Q8nul1 staphylococ
644	3	8.8	33	16	Q8KG99	Q8kg99 chlorobium
645	3	8.8	33	16	Q8FZ67	Q8fz67 brucella su
646	3	8.8	33	16	Q8FYR6	Q8fyr6 brucella su
647	3	8.8	33	16	Q8FY86	Q8fy86 brucella su
648	3	8.8	33	16	Q8EJH6	Q8ejh6 shewanella
649	3	8.8	33	16	Q8EGA9	Q8ega9 shewanella
650	3	8.8	33	16	Q8EE59	Q8ee59 shewanella
651	3	8.8	33	16	Q8EE42	Q8ee42 shewanella
652	3	8.8	33	16	Q8E8W4	Q8e8w4 shewanella
653	3	8.8	33	16	Q8E1Y5	Q8ely5 streptococc
654	3	8.8	33	16	Q8CQY7	Q8cqy7 staphylococ
655	3	8.8	33	17	Q9HSX6	Q9hsx6 halobacteri
656	3	8.8	33	17	Q8U2X8	Q8u2x8 pyrococcus
657	3	8.8	34	2	Q54427	Q54427 spiroplasma
658	3	8.8	34	2	Q9X3L6	Q9x3l6 prochloroco
659	3	8.8	34	2	Q9R5U1	Q9r5u1 campylobact
660	3	8.8	34	2	Q50998	Q50998 neisseria g
661	3	8.8	34	2	Q44208	Q44208 pseudomonas
662	3	8.8	34	2	Q9X7J6	Q9x7j6 pseudomonas
663	3	8.8	34	2	O31061	O31061 butyrivibri
664	3	8.8	34	2	Q9R8A2	Q9r8a2 chlamydia t
665	3	8.8	34	2	Q8GJC8	Q8gjc8 campylobact
666	3	8.8	34	2	Q8G8C9	Q8g8c9 pseudomonas
667	3	8.8	34	3	Q00377	Q00377 coccidioide
668	3	8.8	34	4	Q99910	Q99910 homo sapien
669	3	8.8	34	4	Q9H3R8	Q9h3r8 homo sapien
670	3	8.8	34	4	Q9UI64	Q9ui64 homo sapien
671	3	8.8	34	4	Q8WW51	Q8ww51 homo sapien
672	3	8.8	34	4	Q9BSP7	Q9bsp7 homo sapien
673	3	8.8	34	4	Q9H4L8	Q9h4l8 homo sapien
674	3	8.8	34	4	Q8NEQ3	Q8neq3 homo sapien
675	3	8.8	34	4	Q15251	Q15251 homo sapien
676	3	8.8	34	4	Q9NQY9	Q9nqy9 homo sapien
677	3	8.8	34	5	Q9BIP7	Q9bip7 cooperia pu
678	3	8.8	34	5	Q27821	Q27821 trichomonas
679	3	8.8	34	5	Q9GQE5	Q9gqe5 branchiosto
680	3	8.8	34	5	Q8N063	Q8n063 plasmodium
681	3	8.8	34	6	Q9MZD7	Q9mzd7 ovis aries
682	3	8.8	34	6	P79429	P79429 capra hircu
683	3	8.8	34	6	P82908	P82908 bos taurus
684	3	8.8	34	8	Q9T2H1	Q9t2h1 cyanidium c

685	3	8.8	34	8	O79025	O79025 enallagma v
686	3	8.8	34	8	Q8MCA2	Q8mca2 phaseolus a
687	3	8.8	34	8	Q8HKE1	Q8hke1 rhipicephal
688	3	8.8	34	10	Q8W2H0	Q8w2h0 paspalum no
689	3	8.8	34	10	Q9LKP4	Q9lkp4 elaeis guin
690	3	8.8	34	10	Q8VWL0	Q8vw10 paspalum no
691	3	8.8	34	10	Q9SCA3	Q9sca3 lycopersico
692	3	8.8	34	11	Q923Z1	Q923z1 mus musculu
693	3	8.8	34	11	Q8R557	Q8r557 mus musculu
694	3	8.8	34	11	Q9ET72	Q9et72 mus musculu
695	3	8.8	34	11	Q99KM9	Q99km9 mus musculu
696	3	8.8	34	11	Q99KX7	Q99kx7 mus musculu
697	3	8.8	34	11	Q64170	Q64170 mus sp. b-r
698	3	8.8	34	11	Q8VHL4	Q8vhl4 rattus norv
699	3	8.8	34	12	Q9DW68	Q9dw68 rat cytomeg
700	3	8.8	34	13	O42521	O42521 scyliorhinu
701	3	8.8	34	13	O13101	O13101 ambystoma m
702	3	8.8	34	13	Q8QGG2	Q8qgg2 oncorhynch
703	3	8.8	34	13	Q8QFM9	Q8qfm9 oncorhynch
704	3	8.8	34	13	O42526	O42526 scyliorhinu
705	3	8.8	34	13	Q9PRE7	Q9pre7 oryzias lat
706	3	8.8	34	13	Q8QGG1	Q8qgg1 oncorhynch
707	3	8.8	34	13	Q8QGF7	Q8qgf7 oncorhynch
708	3	8.8	34	15	O40445	O40445 human immun
709	3	8.8	34	15	Q9WR32	Q9wr32 human immun
710	3	8.8	34	15	Q9W8Y1	Q9w8y1 chimpanzee
711	3	8.8	34	16	O25790	O25790 helicobacte
712	3	8.8	34	16	O50812	O50812 borrelia bu
713	3	8.8	34	16	O50877	O50877 borrelia bu
714	3	8.8	34	16	Q9PGH3	Q9pgh3 xylella fas
715	3	8.8	34	16	Q9PGF8	Q9pgf8 xylella fas
716	3	8.8	34	16	Q9PFA5	Q9pfa5 xylella fas
717	3	8.8	34	16	Q9PDD0	Q9pdd0 xylella fas
718	3	8.8	34	16	Q9KRA8	Q9kra8 vibrio chol
719	3	8.8	34	16	Q9KPW9	Q9kpw9 vibrio chol
720	3	8.8	34	16	Q9KNR8	Q9knr8 vibrio chol
721	3	8.8	34	16	Q9KM63	Q9km63 vibrio chol
722	3	8.8	34	16	Q9K7C6	Q9k7c6 bacillus ha
723	3	8.8	34	16	Q9JY24	Q9jy24 neisseria m
724	3	8.8	34	16	Q9JVP3	Q9jvp3 neisseria m
725	3	8.8	34	16	Q97SF7	Q97sf7 streptococc
726	3	8.8	34	16	Q97PI6	Q97pi6 streptococc
727	3	8.8	34	16	Q9K2B9	Q9k2b9 chlamydia p
728	3	8.8	34	16	Q8X4V1	Q8x4v1 escherichia
729	3	8.8	34	16	Q8U5V2	Q8u5v2 agrobacteri
730	3	8.8	34	16	Q8VIY1	Q8viy1 mycobacteri
731	3	8.8	34	16	Q8RIC7	Q8ric7 fusobacteri
732	3	8.8	34	16	Q8NWX3	Q8nwx3 staphylococ
733	3	8.8	34	16	Q8NV10	Q8nv10 staphylococ
734	3	8.8	34	16	Q8KEQ8	Q8keq8 chlorobium
735	3	8.8	34	16	Q8KEL5	Q8kel5 chlorobium
736	3	8.8	34	16	Q8KDE4	Q8kde4 chlorobium
737	3	8.8	34	16	Q8G2Q2	Q8g2q2 brucella su
738	3	8.8	34	16	Q8F897	Q8f897 leptospira
739	3	8.8	34	16	Q8F830	Q8f830 leptospira
740	3	8.8	34	16	Q8F827	Q8f827 leptospira
741	3	8.8	34	16	Q8F5Y7	Q8f5y7 leptospira

742	3	8.8	34	16	Q8F0V9	Q8f0v9 leptospira
743	3	8.8	34	16	Q8EZR6	Q8ezr6 leptospira
744	3	8.8	34	16	Q8EZ37	Q8ez37 leptospira
745	3	8.8	34	16	Q8EYW8	Q8eyw8 leptospira
746	3	8.8	34	16	Q8EYG6	Q8eyg6 leptospira
747	3	8.8	34	16	Q8EXH6	Q8exh6 leptospira
748	3	8.8	34	16	Q8EXA8	Q8exa8 leptospira
749	3	8.8	34	16	Q8EJ65	Q8ej65 shewanella
750	3	8.8	34	16	Q8EI45	Q8ei45 shewanella
751	3	8.8	34	16	Q8EHU5	Q8ehu5 shewanella
752	3	8.8	34	16	Q8EHK1	Q8ehk1 shewanella
753	3	8.8	34	16	Q8E8Y3	Q8e8y3 shewanella
754	3	8.8	34	16	Q8E8W3	Q8e8w3 shewanella
755	3	8.8	34	16	Q8E173	Q8e173 streptococc
756	3	8.8	34	16	Q8CRY3	Q8cry3 staphylococ
757	3	8.8	34	17	Q8U1I1	Q8uli1 pyrococcus
758	3	8.8	35	2	Q9R624	Q9r624 bacillus su
759	3	8.8	35	2	Q9JPG9	Q9jpg9 neisseria m
760	3	8.8	35	2	Q9R625	Q9r625 bacillus su
761	3	8.8	35	2	Q9X3D6	Q9x3d6 prochloroco
762	3	8.8	35	2	Q9R5I3	Q9r5i3 thermoanaer
763	3	8.8	35	2	Q9FCX4	Q9fcx4 clostridium
764	3	8.8	35	2	Q9XBK0	Q9xbk0 bacillus ce
765	3	8.8	35	2	Q53564	Q53564 neisseria g
766	3	8.8	35	2	Q46537	Q46537 bacteroides
767	3	8.8	35	2	Q9ZG35	Q9zg35 chlamydia t
768	3	8.8	35	2	Q9RHG5	Q9rhg5 bacillus ce
769	3	8.8	35	2	Q9R4A1	Q9r4a1 klebsiella
770	3	8.8	35	2	Q8RKG3	Q8rkg3 clostridium
771	3	8.8	35	2	Q8RIW2	Q8riw2 clostridium
772	3	8.8	35	2	Q9R626	Q9r626 bacillus su
773	3	8.8	35	2	P81927	P81927 lactobacill
774	3	8.8	35	3	Q96UT3	Q96ut3 saccharomyc
775	3	8.8	35	4	Q9BVR9	Q9bvr9 homo sapien
776	3	8.8	35	4	Q13380	Q13380 homo sapien
777	3	8.8	35	4	Q13165	Q13165 homo sapien
778	3	8.8	35	4	Q13828	Q13828 homo sapien
779	3	8.8	35	4	Q13264	Q13264 homo sapien
780	3	8.8	35	4	Q9Y634	Q9y634 homo sapien
781	3	8.8	35	4	Q9BU09	Q9bu09 homo sapien
782	3	8.8	35	4	Q8IU77	Q8iu77 homo sapien
783	3	8.8	35	5	Q27754	Q27754 pisaster oc
784	3	8.8	35	5	Q9BIQ5	Q9biq5 cooperia pu
785	3	8.8	35	5	Q9U780	Q9u780 boophilus a
786	3	8.8	35	5	Q26372	Q26372 tribolium c
787	3	8.8	35	5	Q9U782	Q9u782 boophilus m
788	3	8.8	35	5	Q9TVJ7	Q9tvj7 boophilus m
789	3	8.8	35	5	Q9U783	Q9u783 boophilus m
790	3	8.8	35	5	Q9U784	Q9u784 boophilus m
791	3	8.8	35	5	Q9U781	Q9u781 boophilus m
792	3	8.8	35	5	Q8IF21	Q8if21 trypanosoma
793	3	8.8	35	6	Q95N74	Q95n74 equus cabal
794	3	8.8	35	6	Q9MZA7	Q9mza7 sus scrofa
795	3	8.8	35	8	Q951Q6	Q951q6 protoptilum
796	3	8.8	35	8	Q8W7S9	Q8w7s9 colpomenia
797	3	8.8	35	8	Q9GF85	Q9gf85 ginkgo bilo
798	3	8.8	35	8	Q8W7T0	Q8w7t0 petalonia b

799	3	8.8	35	8	Q8W7S8	Q8w7s8 petalonia f
800	3	8.8	35	8	Q8WE70	Q8we70 miliaria ca
801	3	8.8	35	8	Q8W7S7	Q8w7s7 scytosiphon
802	3	8.8	35	8	Q9GF98	Q9gf98 ceratophyll
803	3	8.8	35	8	Q94P82	Q94p82 corallium r
804	3	8.8	35	8	Q8WEJ7	Q8wej7 cycas circi
805	3	8.8	35	8	Q951S7	Q951s7 anthothela
806	3	8.8	35	8	Q951R1	Q951r1 narella nut
807	3	8.8	35	8	Q951S1	Q951s1 corallium k
808	3	8.8	35	8	Q8WII3	Q8wii3 colpomenia
809	3	8.8	35	8	Q951R3	Q951r3 anthomurice
810	3	8.8	35	8	Q8WIIH9	Q8wih9 scytosiphon
811	3	8.8	35	8	Q8WIIH5	Q8wih5 hydroclathr
812	3	8.8	35	8	Q951S9	Q951s9 protodendro
813	3	8.8	35	8	Q8WII1	Q8wii1 scytosiphon
814	3	8.8	35	8	Q951Q9	Q951q9 narella sp.
815	3	8.8	35	8	Q951S4	Q951s4 paragorgia
816	3	8.8	35	8	Q951R5	Q951r5 corallium s
817	3	8.8	35	10	Q9SPU2	Q9spu2 arabidopsis
818	3	8.8	35	10	Q9MAB1	Q9mab1 arabidopsis
819	3	8.8	35	10	Q9ZUW2	Q9zuw2 arabidopsis
820	3	8.8	35	10	Q9S9G9	Q9s9g9 lycopersico
821	3	8.8	35	10	P92971	P92971 arabidopsis
822	3	8.8	35	10	Q9LV08	Q9lv08 arabidopsis
823	3	8.8	35	10	Q9LQ64	Q9lq64 arabidopsis
824	3	8.8	35	10	Q39297	Q39297 brassica na
825	3	8.8	35	10	Q8RVJ7	Q8rvj7 populus eur
826	3	8.8	35	10	Q9FJ84	Q9fj84 arabidopsis
827	3	8.8	35	10	Q8GUX4	Q8gux4 picea maria
828	3	8.8	35	10	Q8GUX1	Q8gux1 picea maria
829	3	8.8	35	11	Q63397	Q63397 rattus norv
830	3	8.8	35	11	Q9JLA4	Q9jla4 mus musculu
831	3	8.8	35	11	Q60608	Q60608 mus musculu
832	3	8.8	35	11	Q9QV30	Q9qv30 rattus sp.
833	3	8.8	35	11	Q922H5	Q922h5 mus musculu
834	3	8.8	35	11	Q8BK89	Q8bk89 mus musculu
835	3	8.8	35	12	Q90151	Q90151 bombyx mori
836	3	8.8	35	12	Q65380	Q65380 banana bunc
837	3	8.8	35	12	Q83333	Q83333 murine hepa
838	3	8.8	35	12	O55549	O55549 measles vir
839	3	8.8	35	12	Q8BB50	Q8bb50 human papil
840	3	8.8	35	13	Q90XB5	Q90xb5 xenopus lae
841	3	8.8	35	13	P83224	P83224 oxyuranus m
842	3	8.8	35	13	P83225	P83225 oxyuranus s
843	3	8.8	35	13	P83227	P83227 oxyuranus m
844	3	8.8	35	13	P83228	P83228 oxyuranus s
845	3	8.8	35	13	P83229	P83229 oxyuranus s
846	3	8.8	35	13	P83226	P83226 oxyuranus s
847	3	8.8	35	15	Q75981	Q75981 human immun
848	3	8.8	35	15	Q9J3S2	Q9j3s2 human immun
849	3	8.8	35	15	O71950	O71950 human immun
850	3	8.8	35	15	Q9IPY2	Q9ipy2 human immun
851	3	8.8	35	15	Q80574	Q80574 human immun
852	3	8.8	35	15	Q80601	Q80601 human immun
853	3	8.8	35	15	Q8QDX6	Q8qdx6 human immun
854	3	8.8	35	15	Q9QFA0	Q9qfa0 human immun
855	3	8.8	35	15	Q9YM80	Q9ym80 human immun

856	3	8.8	35	15	Q8QDY0	Q8qdy0 human immun
857	3	8.8	35	15	Q75970	Q75970 human immun
858	3	8.8	35	15	Q9YM96	Q9ym96 human immun
859	3	8.8	35	15	Q9YM22	Q9ym22 human immun
860	3	8.8	35	15	Q75990	Q75990 human immun
861	3	8.8	35	15	Q75989	Q75989 human immun
862	3	8.8	35	15	Q9YM67	Q9ym67 human immun
863	3	8.8	35	15	Q77250	Q77250 human immun
864	3	8.8	35	15	Q75955	Q75955 human immun
865	3	8.8	35	15	Q9IPY4	Q9ipy4 human immun
866	3	8.8	35	16	O07593	O07593 bacillus su
867	3	8.8	35	16	Q9KR18	Q9kr18 vibrio chol
868	3	8.8	35	16	Q9KNU1	Q9knu1 vibrio chol
869	3	8.8	35	16	Q9JWX5	Q9jwx5 neisseria m
870	3	8.8	35	16	Q9JV38	Q9jv38 neisseria m
871	3	8.8	35	16	Q9A427	Q9a427 caulobacter
872	3	8.8	35	16	Q9K241	Q9k241 chlamydia p
873	3	8.8	35	16	Q8Z811	Q8z811 salmonella
874	3	8.8	35	16	Q8XZB7	Q8xzb7 ralstonia s
875	3	8.8	35	16	Q8X4F4	Q8x4f4 escherichia
876	3	8.8	35	16	Q8KCA6	Q8kca6 chlorobium
877	3	8.8	35	16	Q8G2D4	Q8g2d4 brucella su
878	3	8.8	35	16	Q8F9H5	Q8f9h5 leptospira
879	3	8.8	35	16	Q8F8D4	Q8f8d4 leptospira
880	3	8.8	35	16	Q8F1W8	Q8f1w8 leptospira
881	3	8.8	35	16	Q8EYH6	Q8eyh6 leptospira
882	3	8.8	35	16	Q8EGT2	Q8egt2 shewanella
883	3	8.8	35	16	Q8EGC0	Q8egc0 shewanella
884	3	8.8	35	16	Q8EG97	Q8eg97 shewanella
885	3	8.8	35	16	Q8EEP3	Q8eep3 shewanella
886	3	8.8	35	16	Q8E9Z1	Q8e9z1 shewanella
887	3	8.8	35	16	Q8DUY1	Q8duy1 streptococc
888	3	8.8	35	17	Q9HMP1	Q9hmp1 halobacteri
889	3	8.8	35	17	Q8ZXX9	Q8zxx9 pyrobaculum
890	3	8.8	36	2	O06954	O06954 salmonella
891	3	8.8	36	2	Q8VTS7	Q8vts7 listeria in
892	3	8.8	36	2	Q9ZG79	Q9zg79 chlamydia t
893	3	8.8	36	2	Q9RHE3	Q9rhe3 pediococcus
894	3	8.8	36	2	Q8VTS5	Q8vts5 listeria we
895	3	8.8	36	2	Q44437	Q44437 agrobacteri
896	3	8.8	36	2	Q9LB55	Q9lb55 helicobacte
897	3	8.8	36	2	Q48507	Q48507 lactococcus
898	3	8.8	36	2	Q99094	Q99094 salmonella
899	3	8.8	36	2	Q9S635	Q9s635 prochloroco
900	3	8.8	36	2	Q8VTR8	Q8vtr8 listeria iv
901	3	8.8	36	2	Q8VTS0	Q8vts0 listeria mo
902	3	8.8	36	2	Q8KYW1	Q8kyw1 uncultured
903	3	8.8	36	2	Q9R4X9	Q9r4x9 azotobacter
904	3	8.8	36	2	Q9X3G2	Q9x3g2 prochloroco
905	3	8.8	36	2	O86086	O86086 shewanella
906	3	8.8	36	2	Q9R536	Q9r536 sphingomona
907	3	8.8	36	2	Q8GRH1	Q8grh1 pectobacter
908	3	8.8	36	3	Q96W36	Q96w36 ophiostoma
909	3	8.8	36	4	Q9UNV7	Q9unv7 homo sapien
910	3	8.8	36	4	Q9P1E9	Q9ple9 homo sapien
911	3	8.8	36	4	Q9UPB7	Q9upb7 homo sapien
912	3	8.8	36	4	Q9UML4	Q9uml4 homo sapien

913	3	8.8	36	4	Q8NE47	Q8ne47	homo sapien
914	3	8.8	36	5	Q9GSY9	Q9gsy9	carcinus ma
915	3	8.8	36	5	Q9NGN1	Q9ngn1	strongyloce
916	3	8.8	36	5	Q27730	Q27730	plasmodium
917	3	8.8	36	5	Q9GNP3	Q9gnp3	caenorhabdi
918	3	8.8	36	5	O01333	O01333	caenorhabdi
919	3	8.8	36	5	Q25781	Q25781	plasmodium
920	3	8.8	36	5	Q8ISR7	Q8isr7	spodoptera
921	3	8.8	36	5	Q8IF69	Q8if69	trypanosoma
922	3	8.8	36	6	O97889	O97889	pongo pygma
923	3	8.8	36	6	Q29059	Q29059	sus scrofa
924	3	8.8	36	6	Q9XT44	Q9xt44	pongo pygma
925	3	8.8	36	6	Q9N1C5	Q9n1c5	bos taurus
926	3	8.8	36	6	O97890	O97890	pan troglod
927	3	8.8	36	6	P79428	P79428	capra hircu
928	3	8.8	36	8	O63675	O63675	emberiza pu
929	3	8.8	36	8	Q9GF81	Q9gf81	gnetum gnem
930	3	8.8	36	8	Q9TIE4	Q9tie4	hydrocotyle
931	3	8.8	36	8	Q9TIF1	Q9tif1	bolax gummi
932	3	8.8	36	8	Q9GFA3	Q9gfa3	cabomba car
933	3	8.8	36	8	Q9GF97	Q9gf97	ceratophyll
934	3	8.8	36	8	Q94VL4	Q94vl4	salmo trutt
935	3	8.8	36	8	Q36303	Q36303	musa schizo
936	3	8.8	36	8	Q9TIF0	Q9tif0	klotzschia
937	3	8.8	36	8	Q94NY5	Q94ny5	salmo salar
938	3	8.8	36	8	Q9GF76	Q9gf76	lactoris fe
939	3	8.8	36	8	Q9MSP9	Q9msp9	nymphaea od
940	3	8.8	36	8	Q9TIF3	Q9tif3	eremocharis
941	3	8.8	36	8	Q9GF74	Q9gf74	liriodendro
942	3	8.8	36	8	Q9TIE2	Q9tie2	aralia chin
943	3	8.8	36	8	Q9TIF2	Q9tif2	azorella tr
944	3	8.8	36	8	Q9GF89	Q9gf89	drimys wint
945	3	8.8	36	8	Q9MSR0	Q9msr0	zamia furfu
946	3	8.8	36	8	O63650	O63650	emberiza sc
947	3	8.8	36	8	Q9TIE3	Q9tie3	hydrocotyle
948	3	8.8	36	8	Q9TIE5	Q9tie5	xanthosia a
949	3	8.8	36	8	Q9GFA9	Q9gfa9	acorus cala
950	3	8.8	36	8	Q8HS50	Q8hs50	ascarina lu
951	3	8.8	36	8	Q8HS46	Q8hs46	austrobaile
952	3	8.8	36	8	Q8HS42	Q8hs42	chloranthus
953	3	8.8	36	8	Q8HS31	Q8hs31	lilium supe
954	3	8.8	36	8	Q8HS27	Q8hs27	magnolia st
955	3	8.8	36	8	Q8HS18	Q8hs18	sagittaria
956	3	8.8	36	8	Q8HKF5	Q8hkf5	rhipicephal
957	3	8.8	36	8	Q8HKC6	Q8hkc6	haemaphysal
958	3	8.8	36	10	Q38977	Q38977	arabidopsis
959	3	8.8	36	10	Q8VY71	Q8vy71	arabidopsis
960	3	8.8	36	11	Q9JMC0	Q9jmc0	rattus norv
961	3	8.8	36	11	Q60937	Q60937	mus musculu
962	3	8.8	36	11	P97598	P97598	rattus norv
963	3	8.8	36	12	Q9IX80	Q9ix80	hepatitis b
964	3	8.8	36	12	Q9QQS6	Q9qqq6	tanapox vir
965	3	8.8	36	12	Q9IX82	Q9ix82	hepatitis b
966	3	8.8	36	12	O90722	O90722	calicivirus
967	3	8.8	36	12	Q83609	Q83609	myxoma viru
968	3	8.8	36	12	Q91CY3	Q91cy3	tt virus. o
969	3	8.8	36	12	Q8QQZ2	Q8qqz2	simian viru

970	3	8.8	36	13	O42264	O42264 xenopus lae
971	3	8.8	36	13	Q9W695	Q9w695 gallus gall
972	3	8.8	36	13	Q8QGS0	Q8qgs0 gallus gall
973	3	8.8	36	15	Q76587	Q76587 human immun
974	3	8.8	36	15	Q80551	Q80551 human immun
975	3	8.8	36	15	Q9YNX9	Q9ynx9 human immun
976	3	8.8	36	15	Q80550	Q80550 human immun
977	3	8.8	36	15	Q80553	Q80553 human immun
978	3	8.8	36	15	O40258	O40258 human immun
979	3	8.8	36	15	Q77664	Q77664 human immun
980	3	8.8	36	16	O25389	O25389 helicobacte
981	3	8.8	36	16	O50686	O50686 borrelia bu
982	3	8.8	36	16	O50969	O50969 borrelia bu
983	3	8.8	36	16	Q9KTV5	Q9ktv5 vibrio chol
984	3	8.8	36	16	Q9KRB3	Q9krb3 vibrio chol
985	3	8.8	36	16	Q9KQ34	Q9kq34 vibrio chol
986	3	8.8	36	16	Q9KPR2	Q9kpr2 vibrio chol
987	3	8.8	36	16	Q9KPQ3	Q9kpp3 vibrio chol
988	3	8.8	36	16	Q9KLW9	Q9klw9 vibrio chol
989	3	8.8	36	16	Q9K7G3	Q9k7g3 bacillus ha
990	3	8.8	36	16	Q9JTW3	Q9jtw3 neisseria m
991	3	8.8	36	16	Q8Z1T4	Q8z1t4 salmonella
992	3	8.8	36	16	Q8Z022	Q8z022 anabaena sp
993	3	8.8	36	16	Q8VJ12	Q8vj12 mycobacteri
994	3	8.8	36	16	Q9AGN3	Q9agn3 clostridium
995	3	8.8	36	16	Q8P0H5	Q8p0h5 streptococc
996	3	8.8	36	16	Q8KE95	Q8ke95 chlorobium
997	3	8.8	36	16	Q8KAZ5	Q8kaz5 chlorobium
998	3	8.8	36	16	Q8F9M7	Q8f9m7 leptospira
999	3	8.8	36	16	Q8F8L0	Q8f8l0 leptospira
1000	3	8.8	36	16	Q8F6L6	Q8f6l6 leptospira

ALIGNMENTS

RESULT 1

Q91Y90

ID Q91Y90 PRELIMINARY; PRT; 31 AA.
AC Q91Y90;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Parathyroid hormone (Fragment).
GN PTH.
OS Peromyscus maniculatus (Deer mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Peromyscus.
OX NCBI_TaxID=10042;
RN [1]
RP SEQUENCE FROM N.A.
RA Prince K.L., Dewey M.J.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF382953; AAK63072.1; -.
DR InterPro; IPR001415; Parathyrd_hrm.
DR InterPro; IPR003625; Pthyrhorm_sub.

DR Pfam; PF01279; Parathyroid; 1.
DR ProDom; PD010687; Pthyrhorm_sub; 1.
DR PROSITE; PS00335; PARATHYROID; 1.
FT NON_TER 1 1
FT NON_TER 31 31
SQ SEQUENCE 31 AA; 3461 MW; A208B0E772B9B55B CRC64;

Query Match 26.5%; Score 9; DB 11; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSEIQLMHN 10
|||||||
Db 14 VSEIQLMHN 22

RESULT 2

Q91Y91

ID Q91Y91 PRELIMINARY; PRT; 31 AA.
AC Q91Y91;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Parathyroid hormone (Fragment).
GN PTH.
OS Peromyscus polionotus (Oldfield mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Peromyscus.
OX NCBI_TaxID=42413;
RN [1]
RP SEQUENCE FROM N.A.
RA Prince K.L., Dewey M.J.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF382952; AAK63071.1; -.
DR InterPro; IPR001415; Parathyrd_hrm.
DR InterPro; IPR003625; Pthyrhorm_sub.
DR Pfam; PF01279; Parathyroid; 1.
DR ProDom; PD010687; Pthyrhorm_sub; 1.
DR PROSITE; PS00335; PARATHYROID; 1.
FT NON_TER 1 1
FT NON_TER 31 31
SQ SEQUENCE 31 AA; 3461 MW; A208B0E772B9B55B CRC64;

Query Match 26.5%; Score 9; DB 11; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSEIQLMHN 10
|||||||
Db 14 VSEIQLMHN 22

RESULT 3

O17148

ID O17148 PRELIMINARY; PRT; 34 AA.
AC O17148;

DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Antigen B/1 (Fragment).
 GN AGB/1.
 OS Echinococcus vogeli.
 OC Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda;
 OC Cyclophyllidea; Taeniidae; Echinococcus.
 OX NCBI_TaxID=6213;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94359533; PubMed=8078520;
 RA Frosch P., Hartmann M., Muhlschlegel F., Frosch M.;
 RT "Sequence heterogeneity of the echinococcal antigen B.";
 RL Mol. Biochem. Parasitol. 64:171-175(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Haag K.L., Zaha A., Gottstein B.;
 RT "E. vogeli AgB/1 coding sequence.";
 RL Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF024665; AAB81611.1; -.
 FT NON_TER 1 1
 FT NON_TER 34 34
 SQ SEQUENCE 34 AA; 3964 MW; 3BE894E129CF84F3 CRC64;

Query Match 14.7%; Score 5; DB 5; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKKL 28
 |||||
 Db 15 LRKKL 19

RESULT 4

Q97K50

ID Q97K50 PRELIMINARY; PRT; 34 AA.
 AC Q97K50;
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
 DE Transcriptional regulator, AcrR family.
 GN CAC1071.
 OS Clostridium acetobutylicum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1488;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
 RX MEDLINE=21359325; PubMed=11466286;
 RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
 RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
 RA Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
 RA Bennett G.N., Koonin E.V., Smith D.R.;
 RT "Genome sequence and comparative analysis of the solvent-producing
 bacterium Clostridium acetobutylicum.";

RL J. Bacteriol. 183:4823-4838(2001).

DR EMBL; AE007622; AAK79045.1; -.

KW Complete proteome.

SQ SEQUENCE 34 AA; 4031 MW; 38D1A2A7C2F86E90 CRC64;

Query Match 14.7%; Score 5; DB 16; Length 34;

Best Local Similarity 100.0%; Pred. No. 2.8e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEI 5
|||||
Db 30 SVSEI 34

RESULT 5

Q9HR65

ID Q9HR65 PRELIMINARY; PRT; 34 AA.

AC Q9HR65;

DT 01-MAR-2001 (TrEMBLrel. 16, Created)

DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)

DE Vng0840h.

GN VNG0840H.

OS Halobacterium sp. (strain NRC-1).

OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;

OC Halobacteriaceae; Halobacterium.

OX NCBI_TaxID=64091;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20504483; PubMed=11016950;

RA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,

RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,

RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,

RA Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,

RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,

RA Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,

RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,

RA Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;

RT "Genome sequence of Halobacterium species NRC-1.";

RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).

DR EMBL; AE005025; AAG19293.1; -.

KW Complete proteome.

SQ SEQUENCE 34 AA; 3731 MW; BA957904338DCD45 CRC64;

Query Match 14.7%; Score 5; DB 17; Length 34;

Best Local Similarity 100.0%; Pred. No. 2.8e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKKL 28
|||||
Db 26 LRKKL 30

RESULT 6

Q8BTB9

ID Q8BTB9 PRELIMINARY; PRT; 35 AA.

AC Q8BTB9;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Translin.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Body;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 DR EMBL; AK011220; BAC25325.1; -.
 SQ SEQUENCE 35 AA; 3967 MW; F81156686390ECD8 CRC64;

Query Match 14.7%; Score 5; DB 11; Length 35;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEI 5
 |||||
 Db 2 SVSEI 6

RESULT 7

Q97RG6

ID Q97RG6 PRELIMINARY; PRT; 35 AA.
 AC Q97RG6;
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Hypothetical protein SP0853.
 GN SP0853.
 OS Streptococcus pneumoniae.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1313;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TIGR4;
 RX MEDLINE=21357209; PubMed=11463916;
 RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
 RA Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
 RA Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
 RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
 RA Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,
 RA McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,
 RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
 RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
 RT "Complete genome sequence of a virulent isolate of Streptococcus
 RT pneumoniae.";
 RL Science 293:498-506(2001).

DR EMBL; AE007391; AAK74982.1; -.
DR TIGR; SP0853; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 35 AA; 4276 MW; 6B8813CC028D6C7B CRC64;

Query Match 14.7%; Score 5; DB 16; Length 35;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQD 30
|||||
Db 30 KKLQD 34

RESULT 8

O24285

ID O24285 PRELIMINARY; PRT; 28 AA.
AC O24285;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE LFY protein (Fragment).
GN LFY.
OS Pinus radiata (Monterey pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=3347;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Vegetative;
RA Izquierdo L.Y., Vergara R.F., Alvarez-Buylla E.R.;
RT "Partial characterization of Pinus radiata meristem identity homolog
RT gene (LFY).";
RL Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
DR EMBL; U66725; AAB06792.1; -.
FT NON_TER 1 1
FT NON_TER 28 28
SQ SEQUENCE 28 AA; 3376 MW; 1736738622B4EE74 CRC64;

Query Match 11.8%; Score 4; DB 10; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKK 27
|||||
Db 15 LRKK 18

RESULT 9

Q49148

ID Q49148 PRELIMINARY; PRT; 29 AA.
AC Q49148;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE PQQ biosynthesis polypeptide.
GN PQQD.

OS Methylobacterium extorquens.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Methylobacteriaceae; Methylobacterium.
 OX NCBI_TaxID=408;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AM1;
 RX MEDLINE=94179111; PubMed=8132470;
 RA Morris C.J., Biville F., Turlin E., Lee E., Ellermann K., Fan W.H.,
 RA Ramamoorthi R., Springer A.L., Lidstrom M.E.;
 RT "Isolation, phenotypic characterization, and complementation analysis
 RT of mutants of Methylobacterium extorquens AM1 unable to synthesize
 RT pyrroloquinoline quinone and sequences of pqqD, pqqG, and pqqC.";
 RL J. Bacteriol. 176:1746-1755(1994).
 DR EMBL; L25889; AAA17878.1; -.
 SQ SEQUENCE 29 AA; 3222 MW; B4831562CF76973C CRC64;

Query Match 11.8%; Score 4; DB 2; Length 29;
 Best Local Similarity 100.0%; Pred. No. 3e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSEI 5
 ||||
 Db 8 VSEI 11

RESULT 10 Q9UCL2

ID Q9UCL2 PRELIMINARY; PRT; 29 AA.
 AC Q9UCL2;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Renal intestinal-type alkaline phosphatase (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=93092315; PubMed=1458595;
 RA Nishihara Y., Hayashi Y., Adachi T., Koyama I., Stigbrand T.,
 RA Hirano K.;
 RT "Chemical nature of intestinal-type alkaline phosphatase in human
 RT kidney.";
 RL Clin. Chem. 38:2539-2542(1992).
 DR InterPro; IPR001952; Alk_phosphatase.
 DR ProDom; PD001868; Alk_phosphatase; 1.
 SQ SEQUENCE 29 AA; 3250 MW; 30501BB7BEEAD8D0 CRC64;

Query Match 11.8%; Score 4; DB 4; Length 29;
 Best Local Similarity 100.0%; Pred. No. 3e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29
 ||||
 Db 23 KKLQ 26

RESULT 11

Q25603

ID Q25603 PRELIMINARY; PRT; 29 AA.
 AC Q25603;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Tubulin.
 OS Onchocerca volvulus.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
 OC Onchocercidae; Onchocerca.
 OX NCBI_TaxID=6282;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Chandrashekar R., Curtis K.C., Weil G.J.;
 RT "Onchocerca volvulus cDNA clone."
 RL Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; U15095; AAA50364.1; -.
 SQ SEQUENCE 29 AA; 3539 MW; B917126A923EF884 CRC64;

Query Match 11.8%; Score 4; DB 5; Length 29;
 Best Local Similarity 100.0%; Pred. No. 3e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSEI 5
 ||||
 Db 4 VSEI 7

RESULT 12

Q9TI61

ID Q9TI61 PRELIMINARY; PRT; 29 AA.
 AC Q9TI61;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE Photosystem Q(B) protein (Fragment).
 GN PSBA.
 OS Allosyncarpia ternata.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Myrtales; Myrtaceae; Allosyncarpia.
 OX NCBI_TaxID=34307;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Udovicic F., Ladiges P.Y.;
 RT "Informativeness of nuclear and chloroplast DNA regions and the
 RT phylogeny of the eucalypts and related genera (Myrtaceae).";
 RL Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF190370; AAF15265.1; -.
 KW Chloroplast.
 FT NON_TER 1 1
 SQ SEQUENCE 29 AA; 3501 MW; 977D8E6E67E1D833 CRC64;

Query Match 11.8%; Score 4; DB 8; Length 29;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 31 VHNF 34
|||
Db 7 VHNF 10

RESULT 13

O13043

ID O13043 PRELIMINARY; PRT; 29 AA.
AC O13043;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Whn transcription factor (Fragment).
GN WHN.
OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
OC Scyliorhinidae; Scyliorhinus.
OX NCBI_TaxID=7830;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97268658; PubMed=9108066;
RA Schlake T., Schorpp M., Nehls M., Boehm T.;
RT "The nude gene encodes a sequence-specific DNA binding protein with
RT homologs in organisms that lack an anticipatory immune system.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:3842-3847(1997).
DR EMBL; Y11539; CAA72302.1; -.
DR InterPro; IPR001766; TF_Fork_head.
DR Pfam; PF00250; Fork_head; 1.
DR ProDom; PD000425; TF_Fork_head; 1.
FT NON_TER 1 1
FT NON_TER 29 29
SQ SEQUENCE 29 AA; 3243 MW; 62AE51F2BE7311E2 CRC64;

Query Match 11.8%; Score 4; DB 13; Length 29;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSEI 5
|||
Db 17 VSEI 20

RESULT 14

Q9UBV5

ID Q9UBV5 PRELIMINARY; PRT; 30 AA.
AC Q9UBV5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Intestinal alkaline phosphatase (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=93092315; PubMed=1458595;
 RA Nishihara Y., Hayashi Y., Adachi T., Koyama I., Stigbrand T.,
 RA Hirano K.;
 RT "Chemical nature of intestinal-type alkaline phosphatase in human
 RT kidney.";
 RL Clin. Chem. 38:2539-2542(1992).
 DR InterPro; IPR001952; Alk_phosphatase.
 DR ProDom; PD001868; Alk_phosphatase; 1.
 SQ SEQUENCE 30 AA; 3349 MW; 30501BB7BEB9BDE6 CRC64;

Query Match 11.8%; Score 4; DB 4; Length 30;
 Best Local Similarity 100.0%; Pred. No. 3e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29
 ||||
 Db 24 KKLQ 27

RESULT 15

Q8DZP7

ID Q8DZP7 PRELIMINARY; PRT; 30 AA.
 AC Q8DZP7;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 GN SAG1053.
 OS Streptococcus agalactiae (serotype V).
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=216466;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=2603 V/R / Serotype V;
 RX MEDLINE=22222988; PubMed=12200547;
 RA Tettelin H., Massignani V., Cieslewicz M.J., Eisen J.A., Peterson S.,
 RA Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D.,
 RA Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,
 RA DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,
 RA Radune D., Fedorova N.B., Scanlan D., Khouri H., Mulligan S.,
 RA Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M.,
 RA Iacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Maione D.,
 RA Rinaudo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
 RA Fraser C.M.;
 RT "Complete genome sequence and comparative genomic analysis of an
 RT emerging human pathogen, serotype V Streptococcus agalactiae.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).
 DR EMBL; AE014240; AAM99934.1; -.
 DR TIGR; SAG1053; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 30 AA; 3492 MW; 8BC8F7525007AE91 CRC64;

Query Match 11.8%; Score 4; DB 16; Length 30;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29
 ||||
Db 23 KKLQ 26

RESULT 16

Q55314

ID Q55314 PRELIMINARY; PRT; 31 AA.
AC Q55314;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Urf2 protein (Fragment).
GN URF2.
OS Sulfolobus solfataricus.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=2287;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96085144; PubMed=8521845;
RA Jones C.E., Fleming T.M., Cowan D.A., Littlechild J.A., Piper P.W.;
RT "The phosphoglycerate kinase and glyceraldehyde-3-phosphate
RT dehydrogenase genes from the thermophilic archaeon Sulfolobus
RT solfataricus overlap by 8bp. Isolation, sequencing of the genes and
RT expression on Escherichia coli.";
RL Eur. J. Biochem. 233:800-808(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94082761; PubMed=8259927;
RA Arcari P., Russo A.D., Ianniciello G., Gallo M., Bocchini V.;
RT "Nucleotide sequence and molecular evolution of the gene coding for
RT glyceraldehyde-3-phosphate dehydrogenase in the thermoacidophilic
RT archaeobacterium Sulfolobus solfataricus.";
RL Biochem. Genet. 31:241-251(1993).
DR EMBL; X80178; CAA56461.1; -.
FT NON_TER 31 31
SQ SEQUENCE 31 AA; 3554 MW; 9A2538F911C7309A CRC64;

Query Match 11.8%; Score 4; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 WLRK 26
 ||||
Db 11 WLRK 14

RESULT 17

Q8NEI8

ID Q8NEI8 PRELIMINARY; PRT; 31 AA.
AC Q8NEI8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Hypothetical protein (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Strausberg R.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC030993; AAH30993.1; -.
 KW Hypothetical protein.
 FT NON_TER 1 1
 SQ SEQUENCE 31 AA; 3437 MW; 72DCD0761839F7F7 CRC64;

Query Match 11.8%; Score 4; DB 4; Length 31;
 Best Local Similarity 100.0%; Pred. No. 3.1e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSEI 5
 ||||
 Db 18 VSEI 21

RESULT 18
 O50669

ID O50669 PRELIMINARY; PRT; 31 AA.
 AC O50669;
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Hypothetical protein BBH11.
 GN BBH11.
 OS Borrelia burgdorferi (Lyme disease spirochete).
 OG Plasmid lp28-3.
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
 OX NCBI_TaxID=139;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 35210 / B31;
 RX MEDLINE=98065943; PubMed=9403685;
 RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
 RA Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
 RA Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
 RA Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
 RA van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
 RA Utterback T., Watthey L., McDonald L., Artiach P., Bowman C.,
 RA Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
 RA Smith H.O., Venter J.C.;
 RT "Genomic sequence of a Lyme disease spirochaete, Borrelia
 RT burgdorferi.";
 RL Nature 390:580-586(1997).
 DR EMBL; AE000784; AAC66002.1; -.
 DR TIGR; BBH11; -.
 KW Hypothetical protein; Plasmid; Complete proteome.

SQ SEQUENCE 31 AA; 3892 MW; 8C9F6B9E72D10FBA CRC64;

Query Match 11.8%; Score 4; DB 16; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29

||||

Db 26 KKLQ 29

RESULT 19

Q9QZQ2

ID Q9QZQ2 PRELIMINARY; PRT; 32 AA.
AC Q9QZQ2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Neurotensin receptor (Fragment).
GN NTSR OR NTR1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129;
RX MEDLINE=99445567; PubMed=10514493;
RA Tavares D., Tully K., Dobner P.R.;
RT "Sequences required for induction of neurotensin receptor gene
RT expression during neuronal differentiation of N1E-115 neuroblastoma
RT cells.";
RL J. Biol. Chem. 274:30066-30079(1999).
DR EMBL; AF172326; AAD51806.1; -.
DR MGD; MGI:97386; Ntsr.
KW Receptor.
FT NON_TER 32 32
SQ SEQUENCE 32 AA; 3447 MW; 7F7EA4FA2CCF2EFB CRC64;

Query Match 11.8%; Score 4; DB 11; Length 32;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 HLNS 17

||||

Db 2 HLNS 5

RESULT 20

Q9HSZ0

ID Q9HSZ0 PRELIMINARY; PRT; 32 AA.
AC Q9HSZ0;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Vng0019h.
GN VNG0019H.

OS Halobacterium sp. (strain NRC-1).
 OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
 OC Halobacteriaceae; Halobacterium.
 OX NCBI_TaxID=64091;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20504483; PubMed=11016950;
 RA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
 RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
 RA Swartzell S., Weir D., Hall J., Dahl T.A., Welte R., Goo Y.A.,
 RA Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
 RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
 RA Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
 RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
 RA Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
 RT "Genome sequence of Halobacterium species NRC-1."
 RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
 DR EMBL; AE004971; AAG18659.1; -.
 KW Complete proteome.
 SQ SEQUENCE 32 AA; 3758 MW; 22D669246C97A817 CRC64;

Query Match 11.8%; Score 4; DB 17; Length 32;
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 KLQD 30
 ||||
 Db 13 KLQD 16

RESULT 21
 Q95SD4
 ID Q95SD4 PRELIMINARY; PRT; 33 AA.
 AC Q95SD4;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE GM02640p.
 GN BCDNA:GM02640.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
 RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
 RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY060847; AAL28395.1; -.
 DR FlyBase; FBgn0047288; BcDNA:GM02640.
 SQ SEQUENCE 33 AA; 3720 MW; 9C3FC1AEC9FBE4A7 CRC64;

Query Match 11.8%; Score 4; DB 5; Length 33;

Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29
||||
Db 21 KKLQ 24

RESULT 22

Q9PKX3

ID Q9PKX3 PRELIMINARY; PRT; 33 AA.
AC Q9PKX3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical protein TC0337.
GN TC0337.
OS Chlamydia muridarum.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83560;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MoPn / Nigg;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
RA Eisen J., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
RT pneumoniae AR39.";
RL Nucleic Acids Res. 28:1397-1406(2000).
DR EMBL; AE002301; AAF39200.1; -.
DR TIGR; TC0337; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 33 AA; 4075 MW; 1E7C5AD9BA5371EC CRC64;

Query Match 11.8%; Score 4; DB 16; Length 33;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKK 27
||||
Db 26 LRKK 29

RESULT 23

Q9ZG81

ID Q9ZG81 PRELIMINARY; PRT; 34 AA.
AC Q9ZG81;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE ATP-dependent permease (Fragment).
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=L2 434B;
RA Wang L., Steenburg S.D., Zheng Y., Larsen S.H.;
RT "Gene identification of Chlamydia trachomatis by random DNA
RT sequencing.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF087260; AAD04038.1; -.
FT NON_TER 1 1
FT NON_TER 34 34
SQ SEQUENCE 34 AA; 4186 MW; 3B38196393258A53 CRC64;

Query Match 11.8%; Score 4; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKK 27
|||
Db 25 LRKK 28

RESULT 24

Q8GFK2

ID Q8GFK2 PRELIMINARY; PRT; 34 AA.
AC Q8GFK2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE ORF37.
OS Staphylococcus aureus.
OG Plasmid EDINA plasmid.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E-1;
RA Sugai M., Yamaguchi T., Hayashi T., Nakasone K., Takami H.;
RT "Complete nucleotide sequence of Staphylococcus aureus E-1 EDINA
RT plasmid.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AP003089; BAC54529.1; -.
KW Plasmid.
SQ SEQUENCE 34 AA; 4138 MW; 88FBD773858BC6EE CRC64;

Query Match 11.8%; Score 4; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29
|||
Db 6 KKLQ 9

RESULT 25

Q8C4P4

ID Q8C4P4 PRELIMINARY; PRT; 34 AA.
AC Q8C4P4;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Zinc finger homeodomain 4 (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 DR EMBL; AK081561; BAC38260.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 34 AA; 3755 MW; EF41DCAF348467B0 CRC64;

Query Match 11.8%; Score 4; DB 11; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 KLQD 30
 ||||
 Db 2 KLQD 5

RESULT 26

Q90ZJ4

ID Q90ZJ4 PRELIMINARY; PRT; 34 AA.
 AC Q90ZJ4;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Platelet-derived growth factor A chain long form (Fragment).
 GN PDGF-A.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21363439; PubMed=11470524;
 RA Horiuchi H., Inoue T., Furusawa S., Matsuda H.;
 RT "Characterization and expression of three forms of cDNA encoding
 RT chicken platelet-derived growth factor-A chain.";
 RL Gene 272:181-190(2001).
 DR EMBL; AB031024; BAB62544.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 34 AA; 3983 MW; FEF02F8A45B27DA5 CRC64;

Query Match 11.8%; Score 4; DB 13; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 25 RKKL 28
||||
Db 28 RKKL 31

RESULT 27

Q98FK5

ID Q98FK5 PRELIMINARY; PRT; 34 AA.
AC Q98FK5;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein msr3733.
GN MSR3733.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti.";
RL DNA Res. 7:331-338(2000).
DR EMBL; AP003002; BAB50562.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 34 AA; 3804 MW; D6AAA82ECB590413 CRC64;

Query Match 11.8%; Score 4; DB 16; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 KLQD 30
||||
Db 28 KLQD 31

RESULT 28

Q15421

ID Q15421 PRELIMINARY; PRT; 35 AA.
AC Q15421;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Simian sarcoma associated virus (SSAV)-related pol region DNA
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87071681; PubMed=2431542;
 RA Leib-Mosch C., Brack R., Werner T., Erfle V., Hehlmann R.;
 RT "Isolation of an SSAV-related endogenous sequence from Human DNA.";
 RL Virology 155:666-677(1986).
 DR EMBL; M14911; AAA36592.1; -.
 FT NON_TER 1 1
 FT NON_TER 35 35
 SQ SEQUENCE 35 AA; 3742 MW; 2F70B02EE0BC86DF CRC64;

Query Match 11.8%; Score 4; DB 4; Length 35;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 LQDV 31
 ||||
 Db 6 LQDV 9

RESULT 29

Q8V6J8

ID Q8V6J8 PRELIMINARY; PRT; 35 AA.
 AC Q8V6J8;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Hypothetical 4.1 kDa protein.
 OS Halovirus HF2.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.
 OX NCBI_TaxID=33771;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tang S.-L., Fisher C., Ngui K., Nuttall S.D., Dyll-Smith M.L.;
 RT "Sequence and transcription of halovirus HF2."
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF222060; AAL55025.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 35 AA; 4115 MW; 2652C319622E9CE4 CRC64;

Query Match 11.8%; Score 4; DB 12; Length 35;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSE 4
 ||||
 Db 10 SVSE 13

RESULT 30

Q9KQG4

ID Q9KQG4 PRELIMINARY; PRT; 35 AA.
 AC Q9KQG4;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE Hypothetical protein VC2034.
 GN VC2034.
 OS *Vibrio cholerae*.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; *Vibrio*.
 OX NCBI_TaxID=666;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=El Tor N16961 / Serotype O1;
 RX MEDLINE=20406833; PubMed=10952301;
 RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
 RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
 RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
 RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
 RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
 RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
 RA Fraser C.M.;
 RT "DNA sequence of both chromosomes of the cholera pathogen *Vibrio*
 RT *cholerae*.";
 RL Nature 406:477-483(2000).
 DR EMBL; AE004278; AAF95182.1; -.
 DR TIGR; VC2034; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 35 AA; 4181 MW; D185B6339A711D54 CRC64;

Query Match 11.8%; Score 4; DB 16; Length 35;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29
 ||||
 Db 24 KKLQ 27

RESULT 31

Q8F102
 ID Q8F102 PRELIMINARY; PRT; 35 AA.
 AC Q8F102;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 GN LA3339.
 OS *Leptospira interrogans*.
 OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; *Leptospira*.
 OX NCBI_TaxID=173;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
 RA Ren S.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AE011494; AAN50536.1; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 35 AA; 4253 MW; 0DDFEDFFB32E980B CRC64;

Query Match 11.8%; Score 4; DB 16; Length 35;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 HLNS 17
||||
Db 3 HLNS 6

RESULT 32

Q53920

ID Q53920 PRELIMINARY; PRT; 36 AA.
AC Q53920;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE OrfA protein (Fragment).
GN ORFA.
OS Streptomyces chrysomallus.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1899;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94341259; PubMed=8062824;
RA Pahl A., Keller U.;
RT "Streptomyces chrysomallus FKBP-33 is a novel immunophilin consisting
RT of two FK506-binding domains with its gene transcriptionally coupled
RT to the FKBP-12 gene."
RL EMBO J. 13:3472-3480(1994).
DR EMBL; Z34523; CAA84281.1; -.
DR InterPro; IPR004347; DUF245.
DR Pfam; PF03136; DUF245; 1.
FT NON_TER 1 1
SQ SEQUENCE 36 AA; 4121 MW; EBD470AAF99A728E CRC64;

Query Match 11.8%; Score 4; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 ERVE 22
||||
Db 27 ERVE 30

RESULT 33

O68941

ID O68941 PRELIMINARY; PRT; 36 AA.
AC O68941;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Dinitrogenase 3 beta subunit (Fragment).
GN ANFK.
OS Rhodospirillum rubrum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
OC Rhodospirillaceae; Rhodospirillum.
OX NCBI_TaxID=1085;
RN [1]

RP SEQUENCE FROM N.A.
RA Loveless T.M., Bishop P.E.;
RT "Identification of Genes Unique to Mo-Independent Nitrogenase Systems
RT in Diverse Diazotrophs.";
RL Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF058778; AAC14327.1; -.
DR InterPro; IPR000510; Oxred_nitrognasel.
DR Pfam; PF00148; oxidored_nitro; 1.
FT NON_TER 36 36
SQ SEQUENCE 36 AA; 3957 MW; D94F46BCFD437D97 CRC64;

Query Match 11.8%; Score 4; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKK 27
|||
Db 5 LRKK 8

RESULT 34

Q8WXW8

ID Q8WXW8 PRELIMINARY; PRT; 36 AA.
AC Q8WXW8;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Urea transporter JK glycoprotein (Fragment).
GN JK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Olsson M.L., Irshaid N.M., Eicher N.I., Poole J., Hustinx H.;
RT "Molecular Basis of the Jk(a-b-) Phenotype in Non-Finnish European
RT Pedigrees.";
RL Br. J. Haematol. 0:0-0(2001).
DR EMBL; AF328890; AAL37474.1; -.
DR InterPro; IPR004937; Urea_transporter.
DR Pfam; PF03253; UT; 1.
FT NON_TER 1 1
SQ SEQUENCE 36 AA; 3989 MW; C3A6A964C2F41007 CRC64;

Query Match 11.8%; Score 4; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNSM 18
|||
Db 7 LNSM 10

RESULT 35

Q9SJ63

ID Q9SJ63 PRELIMINARY; PRT; 36 AA.

AC Q9SJ63;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE At2g35870 protein.
 GN AT2G35870.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=20083487; PubMed=10617197;
 RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
 RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
 RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
 RA Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
 RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
 RA Copenhagen G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
 RA Salzberg S.L., Fraser C.M., Venter J.C.;
 RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
 RT thaliana.";
 RL Nature 402:761-768 (1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RA Lin X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AC007017; AAD21470.1; -.
 SQ SEQUENCE 36 AA; 4358 MW; DC966779BBD6B834 CRC64;

Query Match 11.8%; Score 4; DB 10; Length 36;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29
 ||||
 Db 4 KKLQ 7

RESULT 36

Q9PXD1

ID Q9PXD1 PRELIMINARY; PRT; 36 AA.
 AC Q9PXD1;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Genome polyprotein [Contains: envelope glycoprotein E2/NS1 (GP68)]
 DE (Fragment).
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Hepacivirus.
 OX NCBI_TaxID=11103;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=96343121; PubMed=8750162;
 RA Chayama K., Tsubota A., Arase Y., Saitoh S., Ikeda K., Matsumoto T.,
 RA Hashimoto M., Kobayashi M., Kanda M., Morinaga T.;
 RT "Genotype, slow decrease in virus titer during interferon treatment
 RT and high degree of sequence variability of hypervariable region are
 RT indicative of poor response to interferon treatment in patients with
 RT chronic hepatitis type C.";
 RL J. Hepatol. 23:648-653(1995).
 DR InterPro; IPR002531; HCV_NS1.
 DR Pfam; PF01560; HCV_NS1; 1.
 KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
 KW Polyprotein; Transmembrane.
 SQ SEQUENCE 36 AA; 3546 MW; 5BB7935A55048D34 CRC64;

Query Match 11.8%; Score 4; DB 12; Length 36;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 IQLM 8
 ||||
 Db 33 IQLM 36

RESULT 37

Q91D77

ID Q91D77 PRELIMINARY; PRT; 36 AA.
 AC Q91D77;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE ORF2 hypothetical protein, isolate:HM0319 (Fragment).
 OS TTV-like mini virus.
 OC Viruses; ssDNA viruses; Circoviridae.
 OX NCBI_TaxID=93678;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HM0319;
 RA Michitaka K., Matsubara H., Horiike N., Kihana T., Yano M., Mori T.,
 RA Onji M.;
 RT "Existence of TT virus DNA and TTV-like mini virus DNA in infant cord
 RT blood.";
 RL Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AB059561; BAB69654.1; -.
 DR InterPro; IPR004118; TT_ORF2.
 DR Pfam; PF02957; TT_ORF2; 1.
 KW Hypothetical protein.
 FT NON_TER 36 36
 SQ SEQUENCE 36 AA; 4291 MW; 92145F475EA841F1 CRC64;

Query Match 11.8%; Score 4; DB 12; Length 36;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29
 ||||
 Db 14 KKLQ 17

RESULT 38

Q9YHT9

ID Q9YHT9 PRELIMINARY; PRT; 36 AA.
 AC Q9YHT9;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Synaptosome-associated protein 25.2 (Fragment).
 GN SNAP25B OR SNAP.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99057281; PubMed=9843147;
 RA Risinger C., Salaneck E., Soderberg C., Gates M., Postlethwait J.H.,
 RA Larhammar D.;
 RT "Cloning of two loci for synapse protein Snap25 in zebrafish:
 RT comparison of paralogous linkage groups suggests loss of one locus in
 RT the mammalian lineage.";
 RL J. Neurosci. Res. 54:563-573(1998).
 DR EMBL; AF091596; AAC73006.1; -.
 DR ZFIN; ZDB-GENE-980526-392; snap25b.
 FT NON_TER 1 1
 FT NON_TER 36 36
 SQ SEQUENCE 36 AA; 4046 MW; E3434855F7EEC02F CRC64;

Query Match 11.8%; Score 4; DB 13; Length 36;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 ERVE 22
 ||||
 Db 2 ERVE 5

RESULT 39

Q97S91

ID Q97S91 PRELIMINARY; PRT; 36 AA.
 AC Q97S91;
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Hypothetical protein SP0497.
 GN SP0497.
 OS Streptococcus pneumoniae.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1313;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TIGR4;
 RX MEDLINE=21357209; PubMed=11463916;
 RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,

RA Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
 RA Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
 RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
 RA Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,
 RA McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,
 RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
 RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
 RT "Complete genome sequence of a virulent isolate of *Streptococcus*
 RT *pneumoniae*.";
 RL Science 293:498-506(2001).
 DR EMBL; AE007361; AAK74655.1; -.
 DR TIGR; SP0497; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 36 AA; 4282 MW; 749D427D078ACA76 CRC64;

Query Match 11.8%; Score 4; DB 16; Length 36;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29
 ||||
 Db 10 KKLQ 13

RESULT 40

Q8KYJ0

ID Q8KYJ0 PRELIMINARY; PRT; 37 AA.
 AC Q8KYJ0;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Conserved hypothetical protein.
 GN BXA0180.
 OS *Bacillus anthracis*.
 OG Plasmid pX01.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*.
 OX NCBI_TaxID=1392;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A2012;
 RX MEDLINE=22061436; PubMed=12004073;
 RA Read T.D., Salzberg S.L., Pop M., Shumway M., Umayam L., Jiang L.,
 RA Holtzapple E., Busch J.D., Smith K.L., Schupp J.M., Solomon D.,
 RA Keim P., Fraser C.M.;
 RT "Comparative Genome Sequencing for Discovery of Novel Polymorphisms in
 RT *Bacillus anthracis*.";
 RL Science 296:2028-2033(2002).
 DR EMBL; AE011190; AAM26125.1; -.
 KW Hypothetical protein; Plasmid.
 SQ SEQUENCE 37 AA; 4416 MW; B5B11661AC3522BD CRC64;

Query Match 11.8%; Score 4; DB 2; Length 37;
 Best Local Similarity 100.0%; Pred. No. 3.6e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKK 27
 ||||

Db 11 LRKK 14

Search completed: January 14, 2004, 10:41:50
Job time : 29.4206 secs

OM protein - protein search, using sw model

Run on: January 14, 2004, 10:28:19 ; Search time 5.61371 Seconds
 (without alignments)
 284.822 Million cell updates/sec

Title: US-09-843-221A-162
 Perfect score: 34
 Sequence: 1 SVSEIQLMHNRGKHLNSMERVEWLRKKLQDVHNF 34

Scoring table: OLIGO
 Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1319

Minimum DB seq length: 28
 Maximum DB seq length: 40

Post-processing: Listing first 1000 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5	14.7	33	1	FABI_RHASA	P81175 rhamdia sap
2	4	11.8	29	1	DMD_RAT	P11530 rattus norv
3	4	11.8	37	1	SCK2_LEIQH	P45628 leiurus qui
4	4	11.8	39	1	PSBY_SYNY3	P73676 synechocyst
5	4	11.8	39	1	SR1C_SARPE	P08377 sarcophaga
6	3	8.8	28	1	CH60_MYCSM	P80673 mycobacteri
7	3	8.8	28	1	COXB_SOLTU	P80499 solanum tub
8	3	8.8	28	1	GUN_SCHCO	P81190 schizophyll
9	3	8.8	28	1	PA2C_PSEPO	P20260 pseudechis
10	3	8.8	28	1	VIP_ALLMI	P48142 alligator m
11	3	8.8	28	1	VIP_RANRI	P81016 rana ridibu
12	3	8.8	28	1	VIP_SHEEP	P04565 ovis aries
13	3	8.8	29	1	CXOC_CONMA	P37300 conus magus
14	3	8.8	29	1	CXOD_CONMA	Q26350 conus magus
15	3	8.8	29	1	GALA_ALLMI	P47215 alligator m
16	3	8.8	29	1	GALA_AMICA	P47214 amia calva
17	3	8.8	29	1	GALA_CHICK	P30802 gallus gall

18	3	8.8	29	1	GALA_ONCMY	P47213	oncorhynchu
19	3	8.8	29	1	GALA_RANRI	P47216	rana ridibu
20	3	8.8	29	1	GALA_SHEEP	P31234	ovis aries
21	3	8.8	29	1	GLUC_CHIBR	P31297	chinchilla
22	3	8.8	29	1	IPYR_DESVH	P19371	desulfovibr
23	3	8.8	29	1	NUO1_SOLTU	P80267	solanum tub
24	3	8.8	29	1	PCG4_PACGO	P82417	pachycondyl
25	3	8.8	29	1	RS7_METTE	O93639	methanosarc
26	3	8.8	29	1	SODC_OLEEU	P80740	olea europa
27	3	8.8	29	1	TL16_SPIOL	P81834	spinacia ol
28	3	8.8	30	1	CX7A_CONTU	P58923	conus tulip
29	3	8.8	30	1	DMS3_PHYSA	P80279	phyllomedus
30	3	8.8	30	1	FTN_BACFR	P28733	bacteroides
31	3	8.8	30	1	GLUM_ANGAN	P41521	anguilla an
32	3	8.8	30	1	OTCC_AERPU	P11726	aeromonas p
33	3	8.8	30	1	PCCA_MYXXA	P81185	myxococcus
34	3	8.8	30	1	PCG2_PACGO	P82415	pachycondyl
35	3	8.8	30	1	PCG3_PACGO	P82416	pachycondyl
36	3	8.8	30	1	RKGG_LEPKE	P21587	lepidochely
37	3	8.8	30	1	TX2_THRPR	P83476	thrixopelma
38	3	8.8	30	1	UP61_UPEIN	P82037	uperoleia i
39	3	8.8	30	1	UP62_UPEIN	P82038	uperoleia i
40	3	8.8	30	1	VAA2_EQUAR	Q04238	equisetum a
41	3	8.8	30	1	Y523_BORBU	O51473	borrelia bu
42	3	8.8	31	1	CEC1_PIG	P14661	sus scrofa
43	3	8.8	31	1	CXMA_CONMR	P56708	conus marmo
44	3	8.8	31	1	DIUX_DIPPU	P82372	diploptera
45	3	8.8	31	1	H13_WHEAT	P15872	triticum ae
46	3	8.8	31	1	LPL_BUCRP	Q53017	buchnera ap
47	3	8.8	31	1	MALK_PHOLU	P41124	photorhabdu
48	3	8.8	31	1	NAP4_HUMAN	P19877	homo sapien
49	3	8.8	31	1	PETL_LOTJA	Q9bbr4	lotus japon
50	3	8.8	31	1	PETL_MARPO	P12179	marchantia
51	3	8.8	31	1	PETL_MESVI	Q9mun4	mesostigma
52	3	8.8	31	1	PETL_NEPOL	Q9tky9	nephroselmi
53	3	8.8	31	1	SARL_MOUSE	Q9cqd6	mus musculu
54	3	8.8	31	1	SARL_RABIT	P42532	oryctolagus
55	3	8.8	31	1	Y822_BORBU	O51762	borrelia bu
56	3	8.8	32	1	ADHR_DROYA	P28487	drosophila
57	3	8.8	32	1	CAL2_ONCKE	P01264	oncorhynchu
58	3	8.8	32	1	CAL3_ONCKI	P01265	oncorhynchu
59	3	8.8	32	1	CAL_ANGJA	P01262	anguilla ja
60	3	8.8	32	1	COA2_BPIF1	O80296	bacteriopha
61	3	8.8	32	1	CY31_DESAC	P81078	desulfuromo
62	3	8.8	32	1	FF21_SALEN	P55224	salmonella
63	3	8.8	32	1	ITR3_CUCPE	P10293	cucurbita p
64	3	8.8	32	1	ITR4_CUCMA	P07853	cucurbita m
65	3	8.8	32	1	LEC_DOLAX	P02875	dolichos ax
66	3	8.8	32	1	LPID_ECOLI	P03060	escherichia
67	3	8.8	32	1	PETM_GUIITH	O78499	guillardia
68	3	8.8	32	1	PHSS_DESBN	P13064	desulfovibr
69	3	8.8	32	1	PSBQ_PEA	P19589	pisum sativ
70	3	8.8	32	1	PSBT_ODOSI	P49516	odontella s
71	3	8.8	32	1	PSBZ_EUGST	Q8sl89	euglena ste
72	3	8.8	32	1	PSBZ_EUGVI	Q8sl87	euglena vir
73	3	8.8	32	1	Y160_BPT4	P39247	bacteriopha
74	3	8.8	32	1	YCPG_MASLA	P29735	mastigoclad

75	3	8.8	33	1	GLU2_ORENI	P81027	oreochromis
76	3	8.8	33	1	OTCC_PSEPU	P11727	pseudomonas
77	3	8.8	33	1	T1F_PARTE	Q27172	paramecium
78	3	8.8	33	1	YC12_EUGGR	P31559	euglena gra
79	3	8.8	34	1	DMS1_PHYSA	P24302	phyllomedus
80	3	8.8	34	1	DMS2_PHYSA	P80278	phyllomedus
81	3	8.8	34	1	GAST_CAPHI	P04564	capra hircu
82	3	8.8	34	1	GUN1_SCLSC	P21833	sclerotinia
83	3	8.8	34	1	TX1_SCOGR	P56855	scodra gris
84	3	8.8	35	1	CECA_AEDAL	P81417	aedes albop
85	3	8.8	35	1	COPA_CANFA	P40765	canis famil
86	3	8.8	35	1	CPI2_PIG	P80736	sus scrofa
87	3	8.8	35	1	GP58_BPSP1	O48412	bacterioph
88	3	8.8	35	1	HCYA_CHEDE	P83173	cherax dest
89	3	8.8	35	1	LEC1_CYTSE	P22970	cytisis ses
90	3	8.8	35	1	LEC3_ULEEU	P23032	ulex europe
91	3	8.8	35	1	PBP_ORGPS	P34178	orgyia pseu
92	3	8.8	35	1	PETG_CYACA	Q9tlq9	cyanidium c
93	3	8.8	35	1	RL15_SYNP7	P31160	synechococc
94	3	8.8	35	1	SCKK_TITSE	P56219	tityus serr
95	3	8.8	35	1	SCXP_ANDMA	P01498	androctonus
96	3	8.8	35	1	TX1_GRASP	P56852	grammostola
97	3	8.8	35	1	TX1_THRPR	P83480	thrixopelma
98	3	8.8	35	1	TX2_GRASP	P56853	grammostola
99	3	8.8	35	1	TXAG_AGEOP	P31328	agelena opu
100	3	8.8	35	1	VORB_METTM	P80908	methanobact
101	3	8.8	35	1	Y210_HAEIN	P43964	haemophilus
102	3	8.8	35	1	YRKM_BACSU	P54440	bacillus su
103	3	8.8	36	1	ELH_THETS	P80594	theromyzon
104	3	8.8	36	1	NPF_ARTTR	P41334	artioposthi
105	3	8.8	36	1	OSTS_YEAST	Q99380	saccharomyc
106	3	8.8	36	1	PETM_SYNY3	P74810	synechocyst
107	3	8.8	36	1	R18A_BOVIN	P82919	bos taurus
108	3	8.8	36	1	RET4_CHICK	P30370	gallus gall
109	3	8.8	36	1	RL6_HALCU	P05968	halobacteri
110	3	8.8	36	1	SCX1_BUTEU	P15220	buthus eupe
111	3	8.8	36	1	SCXL_LEIQU	P45639	leiurus qui
112	3	8.8	36	1	Y260_BACHD	Q9kg53	bacillus ha
113	3	8.8	36	1	Y609_ARCFU	O29646	archaeoglob
114	3	8.8	37	1	DIU1_TENMO	P56618	tenebrio mo
115	3	8.8	37	1	LCNM_LACLA	P83002	lactococcus
116	3	8.8	37	1	PIP7_BOVIN	P21671	bos taurus
117	3	8.8	37	1	RL36_BACST	P07841	bacillus st
118	3	8.8	37	1	RL36_PASMU	P57942	pasteurella
119	3	8.8	37	1	SCKC_LEIQH	P13487	leiurus qui
120	3	8.8	37	1	SCKI_MESTA	P24663	mesobuthus
121	3	8.8	37	1	Y63_BPT3	P20328	bacterioph
122	3	8.8	38	1	BD08_BOVIN	P46166	bos taurus
123	3	8.8	38	1	CPRP_CANPG	P81033	cancer pagu
124	3	8.8	38	1	HMG2_BOVIN	P40673	bos taurus
125	3	8.8	38	1	MFA2_USTMA	P31963	ustilago ma
126	3	8.8	38	1	NLT1_VITSX	P80275	vitis sp. (
127	3	8.8	38	1	NLT2_VITSX	P33556	vitis sp. (
128	3	8.8	38	1	OBP2_HYSCR	P81648	hystrix cri
129	3	8.8	38	1	PYSA_METBA	P80521	methanosarc
130	3	8.8	38	1	RL36_ECOLI	P21194	escherichia
131	3	8.8	38	1	RL36_PSEAE	Q9hwf6	pseudomonas

132	3	8.8	38	1	RL36_THEMA	Q9xli6	thermotoga
133	3	8.8	38	1	RL36_YERPE	Q8zj91	yersinia pe
134	3	8.8	38	1	RR12_PINCO	P49168	pinus conto
135	3	8.8	38	1	YJ39_ARCFU	O28340	archaeoglob
136	3	8.8	39	1	CEC_GLOMR	P83403	glossina mo
137	3	8.8	39	1	COLI_BALPH	P01195	balaenopter
138	3	8.8	39	1	COLI_RABIT	P06297	oryctolagus
139	3	8.8	39	1	COLI_SQUAC	P01197	squalus aca
140	3	8.8	39	1	COLI_STRCA	P01196	struthio ca
141	3	8.8	39	1	EXE3_HELHO	P20394	heloderma h
142	3	8.8	39	1	FUC3_RAT	P80349	rattus norv
143	3	8.8	39	1	GVPC_SPICC	P81000	spirulina s
144	3	8.8	39	1	H2A_BUFBG	P55897	bufo bufo g
145	3	8.8	39	1	LCGA_LACLA	P36961	lactococcus
146	3	8.8	39	1	PSBX_PORPU	P51197	porphyra pu
147	3	8.8	40	1	ALB1_TRASC	P81188	trachemys s
148	3	8.8	40	1	BD02_BOVIN	P46160	bos taurus
149	3	8.8	40	1	BD07_BOVIN	P46165	bos taurus
150	3	8.8	40	1	BD10_BOVIN	P46168	bos taurus
151	3	8.8	40	1	DEFB_AEDAE	P81602	aedes aegy
152	3	8.8	40	1	HS9A_RABIT	P30946	oryctolagus
153	3	8.8	40	1	KAD_STACA	P35141	staphylococ
154	3	8.8	40	1	PHRK_BACSU	O31840	bacillus su
155	3	8.8	40	1	PRE_BACLI	P18189	bacillus li
156	3	8.8	40	1	RK33_PEA	P51416	pisum sativ
157	3	8.8	40	1	RL36_CORGL	Q8nmn8	corynebacte
158	3	8.8	40	1	RRPO_LSV	P27328	lily sympto
159	3	8.8	40	1	SAPC_SARPE	P31530	sarcophaga
160	3	8.8	40	1	SAUV_PHYSA	P01144	phyllomedus
161	3	8.8	40	1	SR1D_SARPE	P18312	sarcophaga
162	3	8.8	40	1	VIT_MELGA	P56531	meleagris g
163	3	8.8	40	1	YDRB_STRPE	P32012	streptomyce
164	2	5.9	28	1	ACON_CANAL	P82611	candida alb
165	2	5.9	28	1	APC1_RABIT	P33047	oryctolagus
166	2	5.9	28	1	ARYC_NOCGL	P80008	nocardia gl
167	2	5.9	28	1	CIQC_RAT	P31722	rattus norv
168	2	5.9	28	1	ETX2_BACCE	P80568	bacillus ce
169	2	5.9	28	1	FIBA_CANFA	P02673	canis famil
170	2	5.9	28	1	FLA1_TREPH	P21988	treponema p
171	2	5.9	28	1	GDO_TRIMO	P02865	triticum mo
172	2	5.9	28	1	GRP_ALLMI	P31886	alligator m
173	2	5.9	28	1	GTS5_CHICK	P20137	gallus gall
174	2	5.9	28	1	GVPC_OSCAG	P80999	oscillator
175	2	5.9	28	1	HORC_HORSP	P02864	hordeum spo
176	2	5.9	28	1	HSP4_OCTVU	P83216	octopus vul
177	2	5.9	28	1	ICPP_VIPLE	P82475	vipera lebe
178	2	5.9	28	1	IEL1_MOMCH	P10296	momordica c
179	2	5.9	28	1	IORB_METTM	P80911	methanobact
180	2	5.9	28	1	ITR2_MOMCH	P10295	momordica c
181	2	5.9	28	1	ITR3_LUFCY	P35628	luffa cylin
182	2	5.9	28	1	ITRA_MOMCH	P30709	momordica c
183	2	5.9	28	1	LECA_IRIHO	P36230	iris hollan
184	2	5.9	28	1	LPFS_ECOLI	P22183	escherichia
185	2	5.9	28	1	LPL_ECOLI	P09149	escherichia
186	2	5.9	28	1	LPL_SALTI	Q8z9h9	salmonella
187	2	5.9	28	1	LPL_SALTY	P03062	salmonella
188	2	5.9	28	1	LPW_SERMA	P03055	serratia ma

189	2	5.9	28	1	MAAI_RAT	P57113	rattus norv
190	2	5.9	28	1	MCDP_MEGPE	P04567	megabombus
191	2	5.9	28	1	NLT2_WHEAT	P39085	triticum ae
192	2	5.9	28	1	NXL1_BOUAN	P34074	boulengerin
193	2	5.9	28	1	OBP1_HYSCR	P81647	hystrix cri
194	2	5.9	28	1	OMPA_YERPS	P38399	yersinia ps
195	2	5.9	28	1	ORND_PLAOR	P25513	placobdella
196	2	5.9	28	1	OST1_CHICK	P80896	gallus gall
197	2	5.9	28	1	PA22_MICNI	P21791	micrurus ni
198	2	5.9	28	1	PA23_TRIST	P82894	trimeresuru
199	2	5.9	28	1	PETL_CYAPA	P48102	cyanophora
200	2	5.9	28	1	PHR_METTM	P58818	methanobact
201	2	5.9	28	1	PHYB_ASPFI	P81440	aspergillus
202	2	5.9	28	1	PP71_HCMVT	P24429	human cytom
203	2	5.9	28	1	PPOX_BOVIN	P56602	bos taurus
204	2	5.9	28	1	RL5_HALCU	P05972	halobacteri
205	2	5.9	28	1	RS19_PHYS1	O66093	phytoplasma
206	2	5.9	28	1	SCX2_BUTSI	P15230	buthus sind
207	2	5.9	28	1	SLP1_LEIQH	P80669	leiurus qui
208	2	5.9	28	1	SMS2_ORENI	P81029	oreochromis
209	2	5.9	28	1	TXO2_AGEAP	P15971	agelenopsis
210	2	5.9	28	1	VG9_SPV4	P11341	spiroplasma
211	2	5.9	28	1	VIP_DIDMA	P39089	didelphis m
212	2	5.9	28	1	VIP_SCYCA	P09685	scyliorhinu
213	2	5.9	28	1	Y073_ARCFU	O30163	archaeoglob
214	2	5.9	28	1	Y16P_BPT4	P39248	bacterioph
215	2	5.9	28	1	YA79_ARCFU	O29184	archaeoglob
216	2	5.9	29	1	12AH_CLOS4	P21215	clostridium
217	2	5.9	29	1	AL21_HORSE	P81216	equus cabal
218	2	5.9	29	1	AMEL_RABIT	P12761	oryctolagus
219	2	5.9	29	1	ATP9_PICPJ	Q06838	pichia pijp
220	2	5.9	29	1	ATPA_BRYMA	P26965	bryopsis ma
221	2	5.9	29	1	BR2D_RANES	P40840	rana escule
222	2	5.9	29	1	BREE_RANES	P40841	rana escule
223	2	5.9	29	1	CERB_CERCA	P36191	ceratitidis c
224	2	5.9	29	1	COA1_BPI22	P15413	bacterioph
225	2	5.9	29	1	COXJ_CANFA	Q9tr29	canis famil
226	2	5.9	29	1	COXK_SHEEP	Q9tr28	ovis aries
227	2	5.9	29	1	CXD6_CONGL	Q9twm7	conus glori
228	2	5.9	29	1	CXO7_CONGE	P05483	conus geogr
229	2	5.9	29	1	CXST_CONGE	P58844	conus geogr
230	2	5.9	29	1	DMS5_PHYSA	P80281	phyllomedus
231	2	5.9	29	1	GLUC_ANAPL	P01276	anas platyr
232	2	5.9	29	1	GLUC_CALMI	P13189	callorhynch
233	2	5.9	29	1	GLUC_DIDMA	P18108	didelphis m
234	2	5.9	29	1	GLUC_LAMFL	Q9prq9	lampetra fl
235	2	5.9	29	1	GLUC_PLAFE	P23062	platichthys
236	2	5.9	29	1	GLUC_RABIT	P25449	oryctolagus
237	2	5.9	29	1	GLUC_TORMA	P09567	torpedo mar
238	2	5.9	29	1	H2B2_ECHES	P13282	echinus esc
239	2	5.9	29	1	HOXY_RHOOP	P22660	rhodococcus
240	2	5.9	29	1	HRJ_BOTJA	P20416	bothrops ja
241	2	5.9	29	1	HS98_NEUCR	P31540	neurospora
242	2	5.9	29	1	ITH3_BOVIN	P56652	bos taurus
243	2	5.9	29	1	ITR1_CUCMA	P01074	cucurbita m
244	2	5.9	29	1	ITR1_LUFCY	P25849	luffa cylin
245	2	5.9	29	1	ITR1_MOMRE	P17680	momordica r

246	2	5.9	29	1	ITR2_BRYDI	P11968	bryonia dio
247	2	5.9	29	1	ITR3_CYCPE	P83394	cyclanthera
248	2	5.9	29	1	ITR4_CYCPE	P83395	cyclanthera
249	2	5.9	29	1	ITR5_CYCPE	P83396	cyclanthera
250	2	5.9	29	1	MDH_BURPS	P80536	burkholderi
251	2	5.9	29	1	MULR_ECHML	P81798	echis multi
252	2	5.9	29	1	PETN_ANASP	Q913p6	anabaena sp
253	2	5.9	29	1	PETN_ARATH	P12178	arabidopsis
254	2	5.9	29	1	PETN_CHAGL	Q8ma13	chaetosphae
255	2	5.9	29	1	PETN_CYAPA	P48258	cyanophora
256	2	5.9	29	1	PETN_GUIITH	O78498	guillardia
257	2	5.9	29	1	PETN_MAIZE	Q33302	zea mays (m
258	2	5.9	29	1	PETN_MARPO	P12177	marchantia
259	2	5.9	29	1	PETN_MESVI	Q9mus4	mesostigma
260	2	5.9	29	1	PETN_ODOSI	P49527	odontella s
261	2	5.9	29	1	PETN_PINTH	P41611	pinus thunb
262	2	5.9	29	1	PETN_PORPU	P51276	porphyra pu
263	2	5.9	29	1	PETN_PSINU	Q8wi23	psilotum nu
264	2	5.9	29	1	PETN_SYNEL	Q8dkn2	synechococc
265	2	5.9	29	1	PETN_SYNY3	P72717	synechocyst
266	2	5.9	29	1	PK4_DICDI	P34103	dictyosteli
267	2	5.9	29	1	PRO1_DACGL	P18689	dactylis gl
268	2	5.9	29	1	PSAF_SYNPO	P31083	synechococc
269	2	5.9	29	1	PSAK_SPIOL	P14627	spinacia ol
270	2	5.9	29	1	PSAX_SYNPU	P23320	synechococc
271	2	5.9	29	1	PSBI_SYNPU	P12240	synechococc
272	2	5.9	29	1	RL15_HALCU	P05971	halobacteri
273	2	5.9	29	1	RL15_STRLI	P49975	streptomyce
274	2	5.9	29	1	RP54_CLOKL	P38944	clostridium
275	2	5.9	29	1	SCX1_ANDMA	P56215	androctonus
276	2	5.9	29	1	SDHB_CLOPR	P80213	clostridium
277	2	5.9	29	1	SLP2_LEIQH	P80670	leiurus qui
278	2	5.9	29	1	SLP3_LEIQH	P80671	leiurus qui
279	2	5.9	29	1	TAT_HV1Z3	P12510	human immun
280	2	5.9	29	1	TLP_ACTDE	P81370	actinidia d
281	2	5.9	29	1	Y15_BPT7	P03792	bacterioph
282	2	5.9	29	1	Y51_BPT3	P20326	bacterioph
283	2	5.9	29	1	YCX4_ODOSI	P49830	odontella s
284	2	5.9	29	1	YCX4_ODOSI	P49838	odontella s
285	2	5.9	30	1	2ENR_CLOTY	P11887	clostridium
286	2	5.9	30	1	AIAT_CHIVI	P38026	chinchilla
287	2	5.9	30	1	AATC_RABIT	P12343	oryctolagus
288	2	5.9	30	1	AATM_RABIT	P12345	oryctolagus
289	2	5.9	30	1	ACB1_DIGLA	P81624	digitalis l
290	2	5.9	30	1	AMPT_BACST	P00728	bacillus st
291	2	5.9	30	1	ANF_RANRI	P09196	rana ridibu
292	2	5.9	30	1	CALM_LYTPI	P05935	lytechinus
293	2	5.9	30	1	CBAL_BACST	P13722	bacillus st
294	2	5.9	30	1	CH60_CLOPA	P81339	clostridium
295	2	5.9	30	1	CLPA_PINPS	P81671	pinus pinas
296	2	5.9	30	1	COAE_CORAM	P58101	corynebacte
297	2	5.9	30	1	COXC_SOLTU	P80500	solanum tub
298	2	5.9	30	1	CRG2_SCOWA	P19865	scoliodon w
299	2	5.9	30	1	CX2A_CONBE	P58625	conus betul
300	2	5.9	30	1	CXEX_CONCN	P58928	conus conso
301	2	5.9	30	1	CXK4_CONST	P58921	conus stria
302	2	5.9	30	1	CXOB_CONPE	P56713	conus penna

303	2	5.9	30	1	CXVB_CONER	P58783	conus ermin
304	2	5.9	30	1	CY35_DESAC	P81079	desulfuromo
305	2	5.9	30	1	CY01_VIOOD	P82230	viola odora
306	2	5.9	30	1	CY08_VIOOD	P58440	viola odora
307	2	5.9	30	1	DEF2_MACMU	P82317	macaca mula
308	2	5.9	30	1	DIDH_COMTE	P80702	comamonas t
309	2	5.9	30	1	DIU2_HYLLI	P82015	hyles linea
310	2	5.9	30	1	DIU2_MANSE	P24858	manduca sex
311	2	5.9	30	1	END2_ONCKE	P01205	oncorhynchu
312	2	5.9	30	1	FIBR_PANIN	P22775	panulirus i
313	2	5.9	30	1	HCY2_HOMAM	P82297	homarus ame
314	2	5.9	30	1	HSP5_OCTVU	P83217	octopus vul
315	2	5.9	30	1	IHFB_RHILE	P80606	rhizobium l
316	2	5.9	30	1	ITI1_LAGLE	P26771	lagenaria l
317	2	5.9	30	1	ITR1_CITLA	P11969	citrullus l
318	2	5.9	30	1	ITR1_MOMCH	P10294	momordica c
319	2	5.9	30	1	ITR2_ECBEL	P12071	ecballium e
320	2	5.9	30	1	ITR2_LUFCY	P25850	luffa cylin
321	2	5.9	30	1	ITR3_CUCMC	P32041	cucumis mel
322	2	5.9	30	1	ITR3_MOMCO	P82410	momordica c
323	2	5.9	30	1	ITR4_CUCSA	P10292	cucumis sat
324	2	5.9	30	1	ITR6_CYCPE	P83397	cyclanthera
325	2	5.9	30	1	ITR7_CYCPE	P83398	cyclanthera
326	2	5.9	30	1	KAB5_OLDAF	P58456	oldenlandia
327	2	5.9	30	1	LAS1_PIG	P80171	sus scrofa
328	2	5.9	30	1	LEAH_PHAVU	P81870	phaseolus v
329	2	5.9	30	1	MDH_HELGE	P80037	heliobacter
330	2	5.9	30	1	MMAL_DERMI	P16312	dermatophag
331	2	5.9	30	1	NU5M_PISOC	P24999	pisaster oc
332	2	5.9	30	1	NUO2_SOLTU	P80268	solanum tub
333	2	5.9	30	1	P2CO_ARTSP	P37365	arthrobacte
334	2	5.9	30	1	PCG1_PACGO	P82414	pachycondyl
335	2	5.9	30	1	PCG5_PACGO	P82418	pachycondyl
336	2	5.9	30	1	PETN_NEPOL	Q9tl01	nephroselmi
337	2	5.9	30	1	PLF4_RABIT	P83470	oryctolagus
338	2	5.9	30	1	PLMS_SQUAC	P82542	squalus aca
339	2	5.9	30	1	PMGY_CANAL	P82612	candida alb
340	2	5.9	30	1	PRT1_CLUPA	P02335	clupea pall
341	2	5.9	30	1	PRT2_ONCMY	P02331	oncorhynchu
342	2	5.9	30	1	PRT3_ONCMY	P02332	oncorhynchu
343	2	5.9	30	1	PRT4_ONCMY	P02333	oncorhynchu
344	2	5.9	30	1	PRTB_ONCMY	P12819	oncorhynchu
345	2	5.9	30	1	PSAM_CYACA	Q9tlx5	cyanidium c
346	2	5.9	30	1	PSAM_MESVI	Q9mus2	mesostigma
347	2	5.9	30	1	PSAM_ODOSI	P49487	odontella s
348	2	5.9	30	1	PSAM_PINTH	P41601	pinus thunb
349	2	5.9	30	1	PSAM_PORPU	P51395	porphyra pu
350	2	5.9	30	1	PYSD_METBA	P80524	methanosarc
351	2	5.9	30	1	RIPS_MOMCO	P20655	momordica c
352	2	5.9	30	1	RNP_ODOVI	P19640	odocoileus
353	2	5.9	30	1	SCK2_TITSE	P08816	tityus serr
354	2	5.9	30	1	SCX2_CENLI	P18927	centruroide
355	2	5.9	30	1	SILU_RHIPU	P02885	rhizomucor
356	2	5.9	30	1	TAT_HV1ZH	P12512	human immun
357	2	5.9	30	1	TL1X_SPIOL	P82537	spinacia ol
358	2	5.9	30	1	TL29_SPIOL	P81833	spinacia ol
359	2	5.9	30	1	TX2_HETVE	P58426	heteropoda

360	2	5.9	30	1	UC35_MAIZE	P80641	zea mays (m
361	2	5.9	30	1	UDDP_SULAC	P80143	sulfolobus
362	2	5.9	30	1	URE1_ECOLI	Q03284	escherichia
363	2	5.9	30	1	VAA1_EQUAR	Q04236	equisetum a
364	2	5.9	30	1	VAA1_PSINU	Q04237	psilotum nu
365	2	5.9	30	1	VAA2_PSINU	Q04239	psilotum nu
366	2	5.9	30	1	VATN_BOVIN	P81134	bos taurus
367	2	5.9	30	1	VG03_BPPF1	P25137	bacterioph
368	2	5.9	30	1	VPU_HV1SC	P05948	human immun
369	2	5.9	30	1	VTTA_BPT3	P20837	bacterioph
370	2	5.9	30	1	Y161_TREPA	O83196	treponema p
371	2	5.9	30	1	Y357_BORBU	O51332	borrelia bu
372	2	5.9	30	1	Y425_BORBU	O51386	borrelia bu
373	2	5.9	30	1	Y573_TREPA	O83583	treponema p
374	2	5.9	30	1	Y932_TREPA	O83902	treponema p
375	2	5.9	30	1	YCCB_ECOLI	P24244	escherichia
376	2	5.9	31	1	A98A_DROME	O46201	drosophila
377	2	5.9	31	1	BCAM_PIG	O19098	sus scrofa
378	2	5.9	31	1	COG5_BOVIN	P83437	bos taurus
379	2	5.9	31	1	COX4_NEUCR	P06809	neurospora
380	2	5.9	31	1	CTRP_PENMO	P35002	penaeus mon
381	2	5.9	31	1	CXD6_CONNI	P56710	conus nigro
382	2	5.9	31	1	CXG6_CONTE	P58922	conus texti
383	2	5.9	31	1	DEJP_DROME	P81160	drosophila
384	2	5.9	31	1	EFTU_STRLU	P52390	streptomyce
385	2	5.9	31	1	ENDB_CAMDR	P01203	camelus dro
386	2	5.9	31	1	ER29_BOVIN	P81623	bos taurus
387	2	5.9	31	1	ETFD_PARDE	P55932	paracoccus
388	2	5.9	31	1	FBRL_RAT	P22509	rattus norv
389	2	5.9	31	1	FIBB_CANFA	P02677	canis famil
390	2	5.9	31	1	GP37_BPSP1	O48393	bacterioph
391	2	5.9	31	1	GT_SERMA	P22416	serratia ma
392	2	5.9	31	1	HBA_MACEU	P81043	macropus eu
393	2	5.9	31	1	HCY1_HOMAM	P82296	homarus ame
394	2	5.9	31	1	HCY2_MAISQ	P82303	maia squina
395	2	5.9	31	1	HEM2_PHAGO	P27687	phascolopsi
396	2	5.9	31	1	LC70_LACPA	P80959	lactobacill
397	2	5.9	31	1	LCCB_LEUME	P81052	leuconostoc
398	2	5.9	31	1	LPRM_ECOLI	P10739	escherichia
399	2	5.9	31	1	MDH_STRAR	P19982	streptomyce
400	2	5.9	31	1	PETL_ANASP	Q8yvq2	anabaena sp
401	2	5.9	31	1	PETL_ARATH	P56776	arabidopsis
402	2	5.9	31	1	PETL_BETVU	P46612	beta vulgar
403	2	5.9	31	1	PETL_CHLVU	P56306	chlorella v
404	2	5.9	31	1	PETL_GUITH	O78468	guillardia
405	2	5.9	31	1	PETL_MAIZE	P19445	zea mays (m
406	2	5.9	31	1	PETL_ODOSI	P49524	odontella s
407	2	5.9	31	1	PETL_OENHO	Q9mtk4	oenothera h
408	2	5.9	31	1	PETL_ORYSA	P12180	oryza sativ
409	2	5.9	31	1	PETL_PORPU	P51221	porphyra pu
410	2	5.9	31	1	PETL_PSINU	Q8wi03	psilotum nu
411	2	5.9	31	1	PETL_SPIOL	Q9m310	spinacia ol
412	2	5.9	31	1	PETL_WHEAT	P58247	triticum ae
413	2	5.9	31	1	PETM_CYACA	Q9t1r5	cyanidium c
414	2	5.9	31	1	PETN_CYACA	Q9t1r6	cyanidium c
415	2	5.9	31	1	PRT2_CLUPA	P02336	clupea pall
416	2	5.9	31	1	PSAK_ANAVA	P23317	anabaena va

417	2	5.9	31	1	PSAM_CYAPA	P48185	cyanophora
418	2	5.9	31	1	PSAM_EUGGR	P31479	euglena gra
419	2	5.9	31	1	PSBK_SYNVU	P19054	synechococc
420	2	5.9	31	1	PSBM_MESVI	Q9muq7	mesostigma
421	2	5.9	31	1	PSBT_CHLRE	P37256	chlamydomon
422	2	5.9	31	1	PSBT_CHLVU	P56327	chlorella v
423	2	5.9	31	1	PSBT_CYAPA	P48109	cyanophora
424	2	5.9	31	1	PSBT_EUGGR	P20176	euglena gra
425	2	5.9	31	1	PSBT_MESVI	Q9muv6	mesostigma
426	2	5.9	31	1	PSBT_PORPU	P51323	porphyra pu
427	2	5.9	31	1	PYSG_METBA	P80523	methanosarc
428	2	5.9	31	1	RECX_METCL	P37865	methylomona
429	2	5.9	31	1	RL21_STRTR	P48956	streptococc
430	2	5.9	31	1	SARL_HUMAN	O00631	homo sapien
431	2	5.9	31	1	SC37_MESMA	P83407	mesobuthus
432	2	5.9	31	1	SCK5_ANDMA	P31719	androctonus
433	2	5.9	31	1	SCKL_LEIQH	P16341	leiurus qui
434	2	5.9	31	1	SODC_STRHE	P81163	striga herm
435	2	5.9	31	1	TX3_HETVE	P58427	heteropoda
436	2	5.9	31	1	TXA3_PARAC	P09949	parasicyoni
437	2	5.9	31	1	Y191_BORBU	O51209	borrelia bu
438	2	5.9	31	1	Y3KD_BPCHP	P19187	bacterioph
439	2	5.9	31	1	Y603_ARCFU	O29652	archaeoglob
440	2	5.9	32	1	A2M_PACLE	P20738	pacifastacu
441	2	5.9	32	1	APL3_DIAGR	P81471	diatraea gr
442	2	5.9	32	1	ATP0_PIG	P80021	sus scrofa
443	2	5.9	32	1	ATP7_SPIOL	P80088	spinacia ol
444	2	5.9	32	1	ATPO_SPIOL	P80087	spinacia ol
445	2	5.9	32	1	B4G1_RAT	P80225	r beta-1,4-
446	2	5.9	32	1	CAAP_MICEC	P21162	micromonosp
447	2	5.9	32	1	CAL0_BOVIN	P01260	bos taurus
448	2	5.9	32	1	CAL0_PIG	P01259	sus scrofa
449	2	5.9	32	1	CAR1_ECHCA	Q9prp9	echis carin
450	2	5.9	32	1	CEC_OIKKI	P83420	oiketicus k
451	2	5.9	32	1	COA1_BPIF1	O80295	bacterioph
452	2	5.9	32	1	COA1_BPIKE	P03676	bacterioph
453	2	5.9	32	1	COA2_BPFD	P03677	bacterioph
454	2	5.9	32	1	CRP_PLEPL	P12245	pleuronecte
455	2	5.9	32	1	CXG7_CONPE	P56711	conus penna
456	2	5.9	32	1	CYBL_RHOGR	P32953	rhodotorula
457	2	5.9	32	1	DBH_SYNY1	P02343	synechocyst
458	2	5.9	32	1	ER29_CHICK	P81628	gallus gall
459	2	5.9	32	1	ER29_TRIVU	P81629	trichosurus
460	2	5.9	32	1	ERH_PIG	P80230	sus scrofa
461	2	5.9	32	1	FER_PORCR	P18821	porphyridiu
462	2	5.9	32	1	FRIH_ANAPL	P80145	anas platyr
463	2	5.9	32	1	GHR4_RAT	P33581	rattus norv
464	2	5.9	32	1	GLB4_LAMSP	P20413	lamellibrac
465	2	5.9	32	1	GT82_DICLA	P82608	dicentrarch
466	2	5.9	32	1	H2AZ_ONCMY	P22647	oncorhynch
467	2	5.9	32	1	HCYC_CHEDE	P83172	cherax dest
468	2	5.9	32	1	IAAI_AMAHP	P80403	amaranthus
469	2	5.9	32	1	IAPP_BOVIN	Q28207	bos taurus
470	2	5.9	32	1	IAPP_PIG	Q29119	sus scrofa
471	2	5.9	32	1	IAPP_SAGOE	Q28934	saguinus oe
472	2	5.9	32	1	IAPP_SHEEP	Q28605	ovis aries
473	2	5.9	32	1	ILVB_ENTAE	Q09129	enterobacte

474	2	5.9	32	1	ITR2_CUCSA	P10291	cucumis sat
475	2	5.9	32	1	LPID_EDWTA	P08140	edwardsiell
476	2	5.9	32	1	LPIV_ECOLI	P03061	escherichia
477	2	5.9	32	1	MDH_NITAL	P10887	nitzschia a
478	2	5.9	32	1	MIFH_TRITR	P81748	trichuris t
479	2	5.9	32	1	NEUB_PIG	P01297	sus scrofa
480	2	5.9	32	1	OVOS_ANAPL	P20739	anas platyr
481	2	5.9	32	1	P1SM_LOXIN	P83045	loxosceles
482	2	5.9	32	1	PA22_AGKHP	P18997	agkistrodon
483	2	5.9	32	1	PA2_RHONO	P43318	rhopilema n
484	2	5.9	32	1	PETL_CHLRE	P50369	chlamydomon
485	2	5.9	32	1	PETM_PORPU	P51275	porphyra pu
486	2	5.9	32	1	PHNS_DESMU	P13062	desulfovibr
487	2	5.9	32	1	PRI3_ONCMY	P02330	oncorhynchu
488	2	5.9	32	1	PRT1_ESOLU	P02325	esox lucius
489	2	5.9	32	1	PRT1_ONCKE	P02327	oncorhynchu
490	2	5.9	32	1	PRT4_SCYCA	P30259	scyliorhinu
491	2	5.9	32	1	PRT5_ONCMY	P02334	oncorhynchu
492	2	5.9	32	1	PRT6_ONCMY	P08145	oncorhynchu
493	2	5.9	32	1	PRT7_ONCMY	P08146	oncorhynchu
494	2	5.9	32	1	PRT8_ONCMY	P12817	oncorhynchu
495	2	5.9	32	1	PRT9_ONCMY	P08147	oncorhynchu
496	2	5.9	32	1	PRTA_ONCMY	P12818	oncorhynchu
497	2	5.9	32	1	PRTE_HALME	P28308	halobacteri
498	2	5.9	32	1	PRT_ORYLA	Q91185	oryzias lat
499	2	5.9	32	1	PSAM_MARPO	P31590	marchantia
500	2	5.9	32	1	PSBT_CYACA	O19927	cyanidium c
501	2	5.9	32	1	PSBT_GUIITH	O78512	guillardia
502	2	5.9	32	1	PSBZ_EUGAN	Q8sl95	euglena ana
503	2	5.9	32	1	PSBZ_EUGGA	Q8sl93	euglena gra
504	2	5.9	32	1	PSBZ_EUGMY	Q8sl91	euglena myx
505	2	5.9	32	1	RIP2_PHYDI	P34967	phytolacca
506	2	5.9	32	1	RK1_RABIT	P81655	oryctolagus
507	2	5.9	32	1	RS19_YEREN	Q56847	yersinia en
508	2	5.9	32	1	SCK2_CENNO	P58504	centruroide
509	2	5.9	32	1	TAT_SIVM2	P05912	simian immu
510	2	5.9	32	1	TRYP_PENMO	P35050	penaeus mon
511	2	5.9	32	1	TX29_PHONI	P29426	phoneutria
512	2	5.9	32	1	TXP7_APTSC	P49271	aptostichus
513	2	5.9	32	1	UC09_MAIZE	P80615	zea mays (m
514	2	5.9	32	1	Y169_TREPA	O83199	treponema p
515	2	5.9	32	1	Y433_BORBU	O51394	borrelia bu
516	2	5.9	32	1	YH17_HAEIN	P44295	haemophilus
517	2	5.9	32	1	YL55_CAEBL	P34435	caenorhabdi
518	2	5.9	32	1	YSCA_YEREN	Q01242	yersinia en
519	2	5.9	32	1	YTK3_ILTVT	P23985	infectious
520	2	5.9	33	1	ACT_DICVI	Q24733	dictyocaulu
521	2	5.9	33	1	ANP3_MYOSC	P04367	myoxocephal
522	2	5.9	33	1	ANP5_MYOAE	P20421	myoxocephal
523	2	5.9	33	1	ATP7_SOLTU	P80496	solanum tub
524	2	5.9	33	1	BR2A_RANES	P40837	rana escule
525	2	5.9	33	1	BR2B_RANES	P40838	rana escule
526	2	5.9	33	1	BR2E_RANES	P32413	rana escule
527	2	5.9	33	1	BR2_RANBP	P32424	rana brevip
528	2	5.9	33	1	CECB_HELVI	P83414	heliobthis v
529	2	5.9	33	1	CECC_HELVI	P83415	heliobthis v
530	2	5.9	33	1	COA1_BPFD	P03675	bacterioph

531	2	5.9	33	1	COA2_BPI22	P15414	bacterioph
532	2	5.9	33	1	COA2_BPIKE	P03678	bacterioph
533	2	5.9	33	1	COXL_ONCMY	P80330	oncorhynch
534	2	5.9	33	1	CU89_HUMAN	P59042	homo sapien
535	2	5.9	33	1	CXBW_CONRA	P58804	conus radia
536	2	5.9	33	1	CXO_CONVE	P83301	conus ventr
537	2	5.9	33	1	DBB2_DOLAU	P83376	dolabella a
538	2	5.9	33	1	DEF1_MESAU	P81465	mesocricetu
539	2	5.9	33	1	DEF3_MESAU	P81467	mesocricetu
540	2	5.9	33	1	DHE3_PIG	P42174	sus scrofa
541	2	5.9	33	1	FER_PORAE	P18820	porphyridiu
542	2	5.9	33	1	GAST_CAVPO	P06885	cavia porce
543	2	5.9	33	1	GAST_CHIBR	P10034	chinchilla
544	2	5.9	33	1	GAST_DIDMA	P33713	didelphis m
545	2	5.9	33	1	GGN1_RANRU	P80395	rana rugosa
546	2	5.9	33	1	GGN2_RANRU	P80396	rana rugosa
547	2	5.9	33	1	GGN3_RANRU	P80397	rana rugosa
548	2	5.9	33	1	HF40_MAIZE	P82865	zea mays (m
549	2	5.9	33	1	HOXU_RHOOP	P22659	rhodococcus
550	2	5.9	33	1	LPPY_SALTY	P08522	salmonella
551	2	5.9	33	1	LPRH_ECOLI	P37324	escherichia
552	2	5.9	33	1	LYC2_HORSE	P81710	equus cabal
553	2	5.9	33	1	MBP1_MAIZE	P28794	zea mays (m
554	2	5.9	33	1	MHAA_STRCH	P80435	streptomyce
555	2	5.9	33	1	MYMY_MYTED	P81614	mytilus edu
556	2	5.9	33	1	PEN3_ADECU	P35987	canine aden
557	2	5.9	33	1	PETM_CYAPA	P48366	cyanophora
558	2	5.9	33	1	PETM_SYNEL	Q8dj15	synechococc
559	2	5.9	33	1	PK1_DICDI	P34101	dictyosteli
560	2	5.9	33	1	PK5_DICDI	P34104	dictyosteli
561	2	5.9	33	1	PRI1_ONCMY	P02326	oncorhynch
562	2	5.9	33	1	PRI2_ONCMY	P02328	oncorhynch
563	2	5.9	33	1	PRTB_MUGCE	P08130	mugil cepha
564	2	5.9	33	1	PRTL_ECOLI	P02338	escherichia
565	2	5.9	33	1	PSAI_SPIOL	P17228	spinacia ol
566	2	5.9	33	1	PSAK_CUCSA	P42051	cucumis sat
567	2	5.9	33	1	PSBT_ARATH	P37259	arabidopsis
568	2	5.9	33	1	PSBT_MAIZE	P37257	zea mays (m
569	2	5.9	33	1	RL21_XENLA	P49628	xenopus lae
570	2	5.9	33	1	RL26_XENLA	P49629	xenopus lae
571	2	5.9	33	1	RL28_XENLA	P46780	xenopus lae
572	2	5.9	33	1	RL4_HALCU	P05967	halobacteri
573	2	5.9	33	1	RPOC_HETCA	P36441	heterosigma
574	2	5.9	33	1	RRPO_BPBZ1	P09674	bacterioph
575	2	5.9	33	1	RS4_XENLA	P49401	xenopus lae
576	2	5.9	33	1	RT25_BOVIN	P82669	bos taurus
577	2	5.9	33	1	RUGA_RANRU	P80954	rana rugosa
578	2	5.9	33	1	RUGB_RANRU	P80955	rana rugosa
579	2	5.9	33	1	SCX9_BUTOC	P04099	buthus occi
580	2	5.9	33	1	THIO_CLOST	P81109	clostridium
581	2	5.9	33	1	TX1_HETVE	P58425	heteropoda
582	2	5.9	33	1	TXH1_SELHU	P56676	selenocosmi
583	2	5.9	33	1	TXN3_SELHA	P83464	selenocosmi
584	2	5.9	33	1	VT1B_RAT	P58200	rattus norv
585	2	5.9	33	1	Y474_BORBU	O51430	borrelia bu
586	2	5.9	33	1	Y50A_MYCTU	Q9cb56	mycobacteri
587	2	5.9	33	1	Y656_TREPA	O83662	treponema p

588	2	5.9	33	1	Y849_BORBU	Q51789	borrelia bu
589	2	5.9	33	1	YC12_CHLRE	P50370	chlamydomon
590	2	5.9	33	1	YC12_MARPO	P31560	marchantia
591	2	5.9	33	1	YC12_MESVI	Q9mus3	mesostigma
592	2	5.9	33	1	YC12_NEPOL	Q9tky6	nephroselmi
593	2	5.9	33	1	YC12_PINTH	P41600	pinus thunb
594	2	5.9	33	1	YL74_ARCFU	O28108	archaeoglob
595	2	5.9	33	1	YLCH_BP82	Q37869	bacterioph
596	2	5.9	33	1	YLCH_ECOLI	Q47268	escherichia
597	2	5.9	34	1	AMP2_CHICK	P80390	gallus gall
598	2	5.9	34	1	ASPG_PIG	P30918	sus scrofa
599	2	5.9	34	1	BR2C_RANES	P40839	rana escule
600	2	5.9	34	1	BUTH_ANDAU	P56685	androctonus
601	2	5.9	34	1	COL_CHICK	P11148	gallus gall
602	2	5.9	34	1	COXA_THETH	P82543	thermus the
603	2	5.9	34	1	COXG_THUOB	P80976	thunnus obe
604	2	5.9	34	1	CXGS_CONGE	P15472	conus geogr
605	2	5.9	34	1	DEF2_RABIT	P07468	oryctolagus
606	2	5.9	34	1	DEF7_RABIT	P80223	oryctolagus
607	2	5.9	34	1	ECAB_ECTTU	P49344	ectatomma t
608	2	5.9	34	1	EF2_RABIT	P55823	oryctolagus
609	2	5.9	34	1	EGGR_APLCA	P01363	aplysia cal
610	2	5.9	34	1	H1S_STRPU	P19376	strongyloce
611	2	5.9	34	1	HS7S_CUCMA	P31082	cucurbita m
612	2	5.9	34	1	ITR1_MOMCO	P82408	momordica c
613	2	5.9	34	1	ITR2_MOMCO	P82409	momordica c
614	2	5.9	34	1	LPTN_PROVU	P28779	proteus vul
615	2	5.9	34	1	M44E_HUMAN	Q96pgl	homo sapien
616	2	5.9	34	1	MYTA_MYTED	P81612	mytilus edu
617	2	5.9	34	1	MYTB_MYTED	P81613	mytilus edu
618	2	5.9	34	1	PETM_ANASP	Q9f4w2	anabaena sp
619	2	5.9	34	1	PRT1_SAROR	P25327	sarda orien
620	2	5.9	34	1	PRT1_SCOSC	P83264	scomber sco
621	2	5.9	34	1	PRT1_THUTH	P02321	thunnus thy
622	2	5.9	34	1	PRT2_SCOSC	P83265	scomber sco
623	2	5.9	34	1	PRT2_THUTH	P02322	thunnus thy
624	2	5.9	34	1	PRT_DICLA	Q9ps27	dicentrarch
625	2	5.9	34	1	PRT_PERFV	P29629	perca flave
626	2	5.9	34	1	PSAI_LOTJA	Q9bbs0	lotus japon
627	2	5.9	34	1	PSAI_OENHO	Q9mtl2	oenothera h
628	2	5.9	34	1	PSAI_SOYBN	P49159	glycine max
629	2	5.9	34	1	PSBM_ARATH	P12169	arabidopsis
630	2	5.9	34	1	PSBM_CHAGL	Q8ma15	chaetosphae
631	2	5.9	34	1	PSBM_CHLRE	P92277	chlamydomon
632	2	5.9	34	1	PSBM_MAIZE	P48189	zea mays (m
633	2	5.9	34	1	PSBM_MARPO	P12168	marchantia
634	2	5.9	34	1	PSBM_NEPOL	Q9tl37	nephroselmi
635	2	5.9	34	1	PSBM_OENHO	Q9mtm8	oenothera h
636	2	5.9	34	1	PSBM_PEA	P34833	pisum sativ
637	2	5.9	34	1	PSBM_PSINU	Q8wi22	psilotum nu
638	2	5.9	34	1	PSBM_WHEAT	Q9xps6	triticum ae
639	2	5.9	34	1	PSBT_TOBAC	P12184	nicotiana t
640	2	5.9	34	1	PSPC_BOVIN	P15783	bos taurus
641	2	5.9	34	1	PSPC_CANFA	P22397	canis famil
642	2	5.9	34	1	PYSB_METBA	P80522	methanosarc
643	2	5.9	34	1	RNL1_PIG	P15466	sus scrofa
644	2	5.9	34	1	RR2_OCHNE	Q40606	ochrosphaer

645	2	5.9	34	1	SCXM_SCOMA	P80719	scorpio mau
646	2	5.9	34	1	SMS_MYXGL	P19209	myxine glut
647	2	5.9	34	1	THEM_MALSU	P13858	malbranchea
648	2	5.9	34	1	TX33_PHONI	P81789	phoneutria
649	2	5.9	34	1	TXP5_BRASM	P49266	brachypelma
650	2	5.9	34	1	VLYS_BPM1	P08229	bacterioph
651	2	5.9	34	1	VPU_HV1W2	P08808	human immun
652	2	5.9	34	1	Y05J_BPT4	P39239	bacterioph
653	2	5.9	34	1	Y224_TREPA	O83253	treponema p
654	2	5.9	34	1	Y848_BORBU	O51788	borrelia bu
655	2	5.9	34	1	Y870_HAEIN	P44065	haemophilus
656	2	5.9	34	1	Y967_HAEIN	P44086	haemophilus
657	2	5.9	34	1	YC12_GUITH	O78460	guillardia
658	2	5.9	34	1	YC12_ODOSI	P49529	odontella s
659	2	5.9	34	1	YC12_PORPU	P51385	porphyra pu
660	2	5.9	34	1	YC12_SKECO	O96797	skeletonema
661	2	5.9	34	1	YMIA_AGRTU	P38437	agrobacteri
662	2	5.9	34	1	Z33B_HUMAN	Q06731	homo sapien
663	2	5.9	35	1	ADO1_AGRDO	P58608	agriosphodr
664	2	5.9	35	1	C550_BACHA	P80091	bacillus ha
665	2	5.9	35	1	CEC4_BOMMO	P14666	bombyx mori
666	2	5.9	35	1	CECA_HELVI	P83413	heliiothis v
667	2	5.9	35	1	CECB_ANTPE	P01509	antheraea p
668	2	5.9	35	1	CHI1_CASSA	P29137	castanea sa
669	2	5.9	35	1	D3HI_RABIT	P32185	oryctolagus
670	2	5.9	35	1	DEFB_MYTED	P81611	mytilus edu
671	2	5.9	35	1	END4_YEREN	P42691	yersinia en
672	2	5.9	35	1	ERFK_KLEAE	Q08599	klebsiella
673	2	5.9	35	1	EXE2_HELVS	P04204	heloderma s
674	2	5.9	35	1	FAS_CAPHI	P08757	capra hircu
675	2	5.9	35	1	FLAV_NOSSM	P35707	nostoc sp.
676	2	5.9	35	1	GBGU_MOUSE	Q61017	mus musculu
677	2	5.9	35	1	GRDB_CLOPU	P55793	clostridium
678	2	5.9	35	1	GUR_GYMSY	P25810	gymnema syl
679	2	5.9	35	1	HMWC_DESGI	P38588	desulfovibr
680	2	5.9	35	1	IAAC_HORVU	P34951	hordeum vul
681	2	5.9	35	1	KPPR_PINPS	P81664	pinus pinas
682	2	5.9	35	1	LCGB_LACIA	P36962	lactococcus
683	2	5.9	35	1	NEF_HV1H3	P05854	human immun
684	2	5.9	35	1	PBP1_LYMDI	P34176	lymantria d
685	2	5.9	35	1	PBP2_LYMDI	P34177	lymantria d
686	2	5.9	35	1	PBP_HYACE	P34175	hyalophora
687	2	5.9	35	1	PHI1_MYTCA	P35422	mytilus cal
688	2	5.9	35	1	PSAI_CYAPA	P48116	cyanophora
689	2	5.9	35	1	PSBM_SYNY3	P72701	synechocyst
690	2	5.9	35	1	PSBT_MARPO	P12182	marchantia
691	2	5.9	35	1	PSBT_OENHO	P37258	oenothera h
692	2	5.9	35	1	PSBT_ORYSA	P12183	oryza sativ
693	2	5.9	35	1	PSBT_PINTH	P41625	pinus thunb
694	2	5.9	35	1	PSPC_PIG	P15785	sus scrofa
695	2	5.9	35	1	RL32_HALCU	P05965	halobacteri
696	2	5.9	35	1	SCKB_PANIM	P55928	pandinus im
697	2	5.9	35	1	SCKG_PANIM	Q10726	pandinus im
698	2	5.9	35	1	SCX1_BUTSI	P15229	buthus sind
699	2	5.9	35	1	SCX5_BUTEU	P15222	buthus eupe
700	2	5.9	35	1	SMS_LAMFL	Q9prro	lampetra fl
701	2	5.9	35	1	SPRC_PIG	P20112	sus scrofa

702	2	5.9	35	1	THPA_THADA	P21381	thaumatococ
703	2	5.9	35	1	TMTX_MESTA	Q9bn12	mesobuthus
704	2	5.9	35	1	TXH4_SELHU	P83303	selenocosmi
705	2	5.9	35	1	TXKS_STOHE	P29187	stoichactis
706	2	5.9	35	1	TXN4_SELHA	P83471	selenocosmi
707	2	5.9	35	1	VL3_PAPVD	P06919	deer papill
708	2	5.9	35	1	VSPA_CERVI	P18692	cerastes vi
709	2	5.9	35	1	WSP7_PINPS	P81086	pinus pinas
710	2	5.9	35	1	Y320_BORBU	O51299	borrelia bu
711	2	5.9	35	1	Y37_BPT3	P20325	bacterioph
712	2	5.9	35	1	Y644_ARCFU	O29613	archaeoglob
713	2	5.9	35	1	Y845_BORBU	O51785	borrelia bu
714	2	5.9	35	1	Y847_BORBU	O51787	borrelia bu
715	2	5.9	35	1	YC12_CYACA	Q9tlx0	cyanidium c
716	2	5.9	35	1	YC69_ARCFU	O28999	archaeoglob
717	2	5.9	35	1	YQB5_CAEEL	Q09258	caenorhabdi
718	2	5.9	36	1	AMPL_PIG	P28839	sus scrofa
719	2	5.9	36	1	ANFV_ANGJA	P22642	anguilla ja
720	2	5.9	36	1	C3L1_BOVIN	P30922	bos taurus
721	2	5.9	36	1	CBBA_NITVU	P37102	nitrobacter
722	2	5.9	36	1	CECD_ANTPE	P01511	antheraea p
723	2	5.9	36	1	CYC7_GEOME	P81894	geobacter m
724	2	5.9	36	1	DESR_DESGI	P00273	desulfovibr
725	2	5.9	36	1	F4RE_METOG	P80951	methanogeni
726	2	5.9	36	1	GLU1_ORENI	P81026	oreochromis
727	2	5.9	36	1	GLUC_HYDCO	P09682	hydrolagus
728	2	5.9	36	1	H1L5_ENSMI	P27203	ensis minor
729	2	5.9	36	1	HBB_PONPY	Q9tt34	pongo pygma
730	2	5.9	36	1	IAA_STRAU	P04082	streptomyce
731	2	5.9	36	1	IOB1_ISYOB	P58609	isyndus obs
732	2	5.9	36	1	KAD_STRGR	P53398	streptomyce
733	2	5.9	36	1	LHG_RHOVI	P04126	rhodopseudo
734	2	5.9	36	1	LYOX_PIG	P45845	sus scrofa
735	2	5.9	36	1	MFA1_YEAST	P34165	saccharomyc
736	2	5.9	36	1	MPG2_DACGL	Q41183	dactylis gl
737	2	5.9	36	1	MYPC_RAT	P56741	rattus norv
738	2	5.9	36	1	NEUH_CARCA	P11975	cardisoma c
739	2	5.9	36	1	NEUY_GADMO	P80167	gadus morhu
740	2	5.9	36	1	NEUY_ONCMY	P29071	oncorhynch
741	2	5.9	36	1	NEUY_RABIT	P09640	oryctolagus
742	2	5.9	36	1	NEUY_RANRI	P29949	rana ridibu
743	2	5.9	36	1	NIFH_ENTAG	P26249	enterobacte
744	2	5.9	36	1	NLTP_PINPI	P26912	pinus pinea
745	2	5.9	36	1	NUCM_SOLTU	P80264	solanum tub
746	2	5.9	36	1	OST2_CHICK	P80897	gallus gall
747	2	5.9	36	1	PAHO_ALLMI	P06305	alligator m
748	2	5.9	36	1	PAHO_ANSAN	P06304	anser anser
749	2	5.9	36	1	PAHO_CERSI	P37999	ceratotheri
750	2	5.9	36	1	PAHO_DIDMA	P18107	didelphis m
751	2	5.9	36	1	PAHO_EQUZE	P38000	equus zebra
752	2	5.9	36	1	PAHO_ERIEU	P41335	erinaceus e
753	2	5.9	36	1	PAHO_LARAR	P41337	larus argen
754	2	5.9	36	1	PAHO_MACMU	P33684	macaca mula
755	2	5.9	36	1	PAHO_RABIT	P41336	oryctolagus
756	2	5.9	36	1	PAHO_RANCA	P15427	rana catesb
757	2	5.9	36	1	PAHO_RANTE	P31229	rana tempor
758	2	5.9	36	1	PAHO_STRCA	P11967	struthio ca

759	2	5.9	36	1	PAHO_TAPPI	P39659	tapirus pin
760	2	5.9	36	1	PGKH_CHLFU	P36232	chlorella f
761	2	5.9	36	1	PSAD_PEA	P20117	pisum sativ
762	2	5.9	36	1	PSAH_PEA	P20121	pisum sativ
763	2	5.9	36	1	PSAI_ANGLY	P28251	angiopteris
764	2	5.9	36	1	PSAI_BRAOL	Q31909	brassica ol
765	2	5.9	36	1	PSAI_CARCL	Q9gdv2	carpobrotus
766	2	5.9	36	1	PSAI_CHAGL	Q8m9x5	chaetosphae
767	2	5.9	36	1	PSAI_CHLVU	P58214	chlorella v
768	2	5.9	36	1	PSAI_CYACA	Q9tm24	cyanidium c
769	2	5.9	36	1	PSAI_GUITH	O78462	guillardia
770	2	5.9	36	1	PSAI_HORVU	P13165	hordeum vul
771	2	5.9	36	1	PSAI_MARPO	P12185	marchantia
772	2	5.9	36	1	PSAI_MESVI	Q9muq4	mesostigma
773	2	5.9	36	1	PSAI_NEPOL	Q9tl12	nephroselmi
774	2	5.9	36	1	PSAI_PICAB	O47040	picea abies
775	2	5.9	36	1	PSAI_PORPU	P51387	porphyra pu
776	2	5.9	36	1	PSAI_PSINU	Q8wi10	psilotum nu
777	2	5.9	36	1	PSAI_SKECO	O96813	skeletonema
778	2	5.9	36	1	PSAI_TOBAC	P12187	nicotiana t
779	2	5.9	36	1	PSAI_WHEAT	P25410	triticum ae
780	2	5.9	36	1	PSBI_ARATH	P09970	arabidopsis
781	2	5.9	36	1	PSBI_HORVU	P25876	hordeum vul
782	2	5.9	36	1	PSBI_MARPO	P09969	marchantia
783	2	5.9	36	1	PSBI_ORYSA	P12161	oryza sativ
784	2	5.9	36	1	PSBI_PINTH	P41599	pinus thunb
785	2	5.9	36	1	PSBI_PSEMZ	P29796	pseudotsuga
786	2	5.9	36	1	PSBM_CHLVU	P56325	chlorella v
787	2	5.9	36	1	PSBM_SYNEL	Q8dha7	synechococc
788	2	5.9	36	1	PSBY_ODOSI	P49543	odontella s
789	2	5.9	36	1	PSBY_PORPU	P51206	porphyra pu
790	2	5.9	36	1	PYY_AMICA	P29205	amia calva
791	2	5.9	36	1	PYY_LEPSP	P09473	lepisosteus
792	2	5.9	36	1	PYY_ONCKI	P09474	oncorhynchu
793	2	5.9	36	1	PYY_PIG	P01305	sus scrofa
794	2	5.9	36	1	PYY_RAJRH	P29206	raja rhina
795	2	5.9	36	1	PYY_RANRI	P29204	rana ridibu
796	2	5.9	36	1	SCK2_CENLL	P45630	centruroide
797	2	5.9	36	1	SCK3_LEIQH	P45660	leiurus qui
798	2	5.9	36	1	SPYY_PHYBI	P80952	phyllomedus
799	2	5.9	36	1	TAEK_ACTEQ	P81897	actinia equ
800	2	5.9	36	1	TERN_PSEUS	P82321	pseudacanth
801	2	5.9	36	1	TLN1_CHICK	P54939	gallus gall
802	2	5.9	36	1	TX1B_AGEAP	P15970	agelenopsis
803	2	5.9	36	1	TX35_PHONI	P81791	phoneutria
804	2	5.9	36	1	TXAM_METSE	P11495	metridium s
805	2	5.9	36	1	TXD3_PARLU	P83258	paracoelote
806	2	5.9	36	1	TXJA_HADVE	P82227	hadronyche
807	2	5.9	36	1	TXJB_HADVE	P82226	hadronyche
808	2	5.9	36	1	Y16L_BPT4	P39244	bacteriopha
809	2	5.9	36	1	Y297_ARCFU	O29945	archaeoglob
810	2	5.9	36	1	Y4KD_BPCHP	P19188	bacteriopha
811	2	5.9	36	1	Y609_BORBU	O51554	borrelia bu
812	2	5.9	36	1	Y619_ARCFU	O29636	archaeoglob
813	2	5.9	36	1	Y699_TREPA	O83697	treponema p
814	2	5.9	36	1	YC12_CYAPA	P48256	cyanophora
815	2	5.9	36	1	YG50_HAEIN	P44281	haemophilus

816	2	5.9	36	1	YRKG_BACSU	P54434	bacillus su
817	2	5.9	37	1	24KD_PLACH	P14592	plasmodium
818	2	5.9	37	1	AFP4_MALPA	P83138	malva parvi
819	2	5.9	37	1	ANP3_PSEAM	P02733	pseudopleur
820	2	5.9	37	1	ATPO_SOLTU	P80504	solanum tub
821	2	5.9	37	1	B2MG_ORENI	Q03423	oreochromis
822	2	5.9	37	1	CAL1_PIG	P30880	sus scrofa
823	2	5.9	37	1	CAL1_SHEEP	P30881	ovis aries
824	2	5.9	37	1	CALR_RANRI	P31888	rana ridibu
825	2	5.9	37	1	CEC2_MANSE	P14662	manduca sex
826	2	5.9	37	1	CEC3_MANSE	P14663	manduca sex
827	2	5.9	37	1	CEC4_MANSE	P14664	manduca sex
828	2	5.9	37	1	CG2S_LUPAN	P09930	lupinus ang
829	2	5.9	37	1	CHCD_ANTPO	P08931	antheraea p
830	2	5.9	37	1	CS40_STAAU	P81684	staphylococ
831	2	5.9	37	1	CUP4_SARBU	P14486	sarcophaga
832	2	5.9	37	1	DEF4_ANDAU	P56686	androctonus
833	2	5.9	37	1	DEFA_MYTED	P81610	mytilus edu
834	2	5.9	37	1	ECAA_ECTTU	P49343	ectatomma t
835	2	5.9	37	1	ES2A_RANES	P40845	rana escule
836	2	5.9	37	1	ES2B_RANES	P40846	rana escule
837	2	5.9	37	1	F13A_BOVIN	P12260	bos taurus
838	2	5.9	37	1	GHR3_RAT	P33580	rattus norv
839	2	5.9	37	1	HCYB_CANPG	P83175	cancer pagu
840	2	5.9	37	1	HOXF_RHOOP	P22658	rhodococcus
841	2	5.9	37	1	IAPP_CRIGR	P19890	cricetulus
842	2	5.9	37	1	LPPY_SERMA	P19937	serratia ma
843	2	5.9	37	1	MAUR_PARVE	Q56462	paracoccus
844	2	5.9	37	1	ME20_EUPRA	P26888	euplotes ra
845	2	5.9	37	1	ME22_EUPRA	P58548	euplotes ra
846	2	5.9	37	1	MIBP_PSESP	P04576	pseudomonas
847	2	5.9	37	1	NLT3_VITSX	P80273	vitis sp. (
848	2	5.9	37	1	NLT4_VITSX	P80274	vitis sp. (
849	2	5.9	37	1	NUFM_SOLTU	P80266	solanum tub
850	2	5.9	37	1	OGT1_RABIT	P81436	oryctolagus
851	2	5.9	37	1	OP2A_OXYKI	P83248	oxyopes kit
852	2	5.9	37	1	OP2B_OXYKI	P83249	oxyopes kit
853	2	5.9	37	1	OP2C_OXYKI	P83250	oxyopes kit
854	2	5.9	37	1	OP2D_OXYKI	P83251	oxyopes kit
855	2	5.9	37	1	PETG_ANASP	P58246	anabaena sp
856	2	5.9	37	1	PETG_ANAVA	Q913p7	anabaena va
857	2	5.9	37	1	PETG_ARATH	P56775	arabidopsis
858	2	5.9	37	1	PETG_CHAGL	Q8m9y4	chaetosphae
859	2	5.9	37	1	PETG_CHLEU	P46304	chlamydomon
860	2	5.9	37	1	PETG_CHLRE	Q08362	chlamydomon
861	2	5.9	37	1	PETG_CHLVU	P56305	chlorella v
862	2	5.9	37	1	PETG_CUSRE	P30398	cuscuta ref
863	2	5.9	37	1	PETG_CYAPA	P14236	cyanophora
864	2	5.9	37	1	PETG_EUGGR	P30396	euglena gra
865	2	5.9	37	1	PETG_GUIITH	O78505	guillardia
866	2	5.9	37	1	PETG_MARPO	P12120	marchantia
867	2	5.9	37	1	PETG_MESVI	Q9mun3	mesostigma
868	2	5.9	37	1	PETG_NEPOL	Q9tky8	nephroselmi
869	2	5.9	37	1	PETG_ODOSI	P49470	odontella s
870	2	5.9	37	1	PETG_ORYSA	P12121	oryza sativ
871	2	5.9	37	1	PETG_PINTH	P41614	pinus thunb
872	2	5.9	37	1	PETG_PORPU	P51318	porphyra pu

873	2	5.9	37	1	PETG_PSINU	Q8wi02	psilotum nu
874	2	5.9	37	1	PETG_SKECO	O96811	skeletonema
875	2	5.9	37	1	PETG_SYNEL	Q8dki2	synechococc
876	2	5.9	37	1	PETG_SYNP7	Q9z3g1	synechococc
877	2	5.9	37	1	PIIL_ACHLY	P81720	achromobact
878	2	5.9	37	1	POLN_WEEV	P13896	western equ
879	2	5.9	37	1	PRF1_RAT	P18889	rattus norv
880	2	5.9	37	1	PRT3_SCYCA	P30258	scyliorhinu
881	2	5.9	37	1	PSAI_ARATH	P56768	arabidopsis
882	2	5.9	37	1	PSAJ_EUGGR	P30394	euglena gra
883	2	5.9	37	1	PSBL_ARATH	P29301	arabidopsis
884	2	5.9	37	1	PSBL_ORYSA	P12166	oryza sativ
885	2	5.9	37	1	PSBM_PINTH	P41608	pinus thunb
886	2	5.9	37	1	PSBY_CYACA	O19893	cyanidium c
887	2	5.9	37	1	PSBY_GUITH	O78433	guillardia
888	2	5.9	37	1	PYY_CHICK	P29203	gallus gall
889	2	5.9	37	1	REV_SIVM2	P08809	simian immu
890	2	5.9	37	1	RK36_ARATH	P12144	arabidopsis
891	2	5.9	37	1	RK36_ASTLO	P24355	astasia lon
892	2	5.9	37	1	RK36_CHAGL	Q8m9v5	chaetosphae
893	2	5.9	37	1	RK36_CHLVU	P56360	chlorella v
894	2	5.9	37	1	RK36_CYACA	Q9tlu9	cyanidium c
895	2	5.9	37	1	RK36_CYAPA	P48131	cyanophora
896	2	5.9	37	1	RK36_EPIVI	P30069	epifagus vi
897	2	5.9	37	1	RK36_EUGGR	P21532	euglena gra
898	2	5.9	37	1	RK36_LOTJA	Q9bbq2	lotus japon
899	2	5.9	37	1	RK36_MARPO	P12142	marchantia
900	2	5.9	37	1	RK36_NEPOL	Q9tl126	nephroselmi
901	2	5.9	37	1	RK36_ODOSI	P49568	odontella s
902	2	5.9	37	1	RK36_OENHO	Q9mtj1	oenothera h
903	2	5.9	37	1	RK36_ORYSA	P12143	oryza sativ
904	2	5.9	37	1	RK36_PEA	P07815	pisum sativ
905	2	5.9	37	1	RK36_PINTH	P41631	pinus thunb
906	2	5.9	37	1	RK36_PORPU	P51296	porphyra pu
907	2	5.9	37	1	RK36_PSINU	Q8why9	psilotum nu
908	2	5.9	37	1	RK36_SPIOL	P12230	spinacia ol
909	2	5.9	37	1	RL36_ANASP	Q8ypk0	anabaena sp
910	2	5.9	37	1	RL36_AQUAE	O66487	aquifex aeo
911	2	5.9	37	1	RL36_BACHD	O50631	bacillus ha
912	2	5.9	37	1	RL36_BACSU	P20278	bacillus su
913	2	5.9	37	1	RL36_BORBU	O51452	borrelia bu
914	2	5.9	37	1	RL36_CAMJE	Q9pm84	campylobact
915	2	5.9	37	1	RL36_CLOAB	Q97ek2	clostridium
916	2	5.9	37	1	RL36_CLOPE	Q8xhu7	clostridium
917	2	5.9	37	1	RL36_DEIRA	Q9rsk0	deinococcus
918	2	5.9	37	1	RL36_HAEIN	P46361	haemophilus
919	2	5.9	37	1	RL36_HELPJ	Q9zjt1	helicobacte
920	2	5.9	37	1	RL36_HELPY	P56058	helicobacte
921	2	5.9	37	1	RL36_LEPIN	Q9xd13	leptospira
922	2	5.9	37	1	RL36_LISMO	Q927n0	listeria mo
923	2	5.9	37	1	RL36_MYCGA	Q9rdv9	mycoplasma
924	2	5.9	37	1	RL36_MYCGE	P47420	mycoplasma
925	2	5.9	37	1	RL36_MYCLE	Q9x7a2	mycobacteri
926	2	5.9	37	1	RL36_MYCPN	P52864	mycoplasma
927	2	5.9	37	1	RL36_MYCPU	Q98q05	mycoplasma
928	2	5.9	37	1	RL36_MYCSP	P38015	mycoplasma
929	2	5.9	37	1	RL36_MYCTU	P45810	mycobacteri

930	2	5.9	37	1	RL36_NEIMA	Q9jrb2	neisseria m
931	2	5.9	37	1	RL36_STAAM	Q99s42	staphylococ
932	2	5.9	37	1	RL36_STRCO	O86772	streptomyce
933	2	5.9	37	1	RL36_SYNP6	O24707	synechococc
934	2	5.9	37	1	RL36_THETH	P80256	thermus the
935	2	5.9	37	1	RL36_THETN	Q8r7x8	thermoanaer
936	2	5.9	37	1	RL36_TREPA	O83239	treponema p
937	2	5.9	37	1	RL36_UREPA	Q9pqn7	ureaplasma
938	2	5.9	37	1	RL36_VIBCH	P78001	vibrio chol
939	2	5.9	37	1	RL7_CLOPA	P05393	clostridium
940	2	5.9	37	1	RS15_HELLU	P52820	helix lucor
941	2	5.9	37	1	RUGC_RANRU	P80956	rana rugosa
942	2	5.9	37	1	SCIT_MESTA	P81761	mesobuthus
943	2	5.9	37	1	SCK3_BUTOC	P59290	buthus occi
944	2	5.9	37	1	SCK3_PARTR	P83112	parabuthus
945	2	5.9	37	1	SCKA_TITSE	P46114	tityus serr
946	2	5.9	37	1	SMS_PETMA	P21779	petromyzon
947	2	5.9	37	1	TCTP_TRYBB	P35758	trypanosoma
948	2	5.9	37	1	THHS_HORVU	P33045	hordeum vul
949	2	5.9	37	1	TX21_SELHU	P82959	selenocosmi
950	2	5.9	37	1	TX22_SELHU	P82960	selenocosmi
951	2	5.9	37	1	TXD1_PARLU	P83256	paracoelote
952	2	5.9	37	1	TXD2_PARLU	P83257	paracoelote
953	2	5.9	37	1	TXD4_PARLU	P83259	paracoelote
954	2	5.9	37	1	TXJC_HADVE	P82228	hadronyche
955	2	5.9	37	1	TXOF_HADVE	P81599	hadronyche
956	2	5.9	37	1	TXP3_APTSC	P49268	aptostichus
957	2	5.9	37	1	VA1_BPBF2	P19347	bacterioph
958	2	5.9	37	1	VG40_BPML5	Q05250	mycobacteri
959	2	5.9	37	1	VG65_BPPH2	P16515	bacterioph
960	2	5.9	37	1	VG65_BPPZA	P08384	bacterioph
961	2	5.9	37	1	VGJ_BPPHX	P03651	bacterioph
962	2	5.9	37	1	VP64_NPVBM	P41722	bombyx mori
963	2	5.9	37	1	VPU_HV1Z8	P08807	human immun
964	2	5.9	37	1	Y268_ARCFU	O29971	archaeoglob
965	2	5.9	37	1	Y63_BPT7	P03799	bacterioph
966	2	5.9	37	1	Y692_BORBU	O51635	borrelia bu
967	2	5.9	37	1	Y700_BORBU	O51643	borrelia bu
968	2	5.9	37	1	Y762_BORBU	O51703	borrelia bu
969	2	5.9	37	1	Y846_BORBU	O51786	borrelia bu
970	2	5.9	37	1	YBGT_ECOLI	P56100	escherichia
971	2	5.9	37	1	YC12_CHLVU	P56328	chlorella v
972	2	5.9	37	1	YDA3_SCHPO	Q10345	schizosacch
973	2	5.9	37	1	YIM4_BPPH1	P10428	bacterioph
974	2	5.9	37	1	YQGE_BACCA	P28753	bacillus ca
975	2	5.9	37	1	YRYL_CAEL	Q19177	caenorhabdi
976	2	5.9	38	1	A2M_HOMAM	P20737	homarus ame
977	2	5.9	38	1	AFP5_MALPA	P83139	malva parvi
978	2	5.9	38	1	BD01_BOVIN	P46159	bos taurus
979	2	5.9	38	1	COA3_XANCP	Q07484	xanthomonas
980	2	5.9	38	1	CRS3_NOTGO	P15534	nototodarus
981	2	5.9	38	1	CU47_LACCU	P80323	lactobacill
982	2	5.9	38	1	DCHS_MICSP	P00863	micrococcus
983	2	5.9	38	1	DEF4_LEIQH	P41965	leiurus qui
984	2	5.9	38	1	DEF7_SPIOL	P81573	spinacia ol
985	2	5.9	38	1	DEFI_AESCY	P80154	aeschna cya
986	2	5.9	38	1	DEFI_MYTGA	P80571	mytilus gal

987	2	5.9	38	1	DLP3_ORNAN	P82141	ornithorhyn
988	2	5.9	38	1	DNP_DENAN	P28374	dendroaspis
989	2	5.9	38	1	DPOB_BOVIN	Q27958	bos taurus
990	2	5.9	38	1	E2F1_RAT	O09139	rattus norv
991	2	5.9	38	1	EST5_DROMO	P10095	drosophila
992	2	5.9	38	1	EXE1_HEL SU	P04203	heloderma s
993	2	5.9	38	1	FER_METPR	P81542	metallospa
994	2	5.9	38	1	GLUM_HYDCO	P23063	hydrolagus
995	2	5.9	38	1	GME1_RAT	Q9quz8	rattus norv
996	2	5.9	38	1	H5_COLLI	P02260	columba liv
997	2	5.9	38	1	HIS1_MACFA	P34084	macaca fasc
998	2	5.9	38	1	HOXH_RHOOP	P22661	rhodococcus
999	2	5.9	38	1	ID5B_ADEPA	P09942	adenanthera
1000	2	5.9	38	1	ID5B_PROJU	P32734	prosopsis j

ALIGNMENTS

RESULT 1

FABI_RHASA

ID FABI_RHASA STANDARD; PRT; 33 AA.

AC P81175;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE Fatty acid-binding protein, intestinal (I-FABP) (FABPI) (Fragments).

OS Rhamdia sapo.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;

OC Pimelodidae; Rhamdia.

OX NCBI_TaxID=55673;

RN [1]

RP SEQUENCE.

RC TISSUE=Intestine;

RX MEDLINE=98036128; PubMed=9370361;

RA Di Pietro S.M., Dell'Angelica E.C., Veerkamp J.H., Sterin-Speziale N.,

RA Santome J.A.;

RT "Amino acid sequence, binding properties and evolutionary

RT relationships of the basic liver fatty-acid-binding protein from the

RT catfish Rhamdia sapo.";

RL Eur. J. Biochem. 249:510-517(1997).

CC -!- FUNCTION: FABP ARE THOUGHT TO PLAY A ROLE IN THE INTRACELLULAR

CC TRANSPORT OF LONG-CHAIN FATTY ACIDS AND THEIR ACYL-COA ESTERS.

CC -!- SUBCELLULAR LOCATION: Cytoplasmic.

CC -!- TISSUE SPECIFICITY: INTESTINE.

CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF

CC TRANSPORTERS.

DR InterPro; IPR000463; Fatty_acid_BP.

DR PROSITE; PS00214; FABP; PARTIAL.

KW Transport; Lipid-binding.

FT	NON_TER	1	1
FT	NON_CONS	12	13
FT	NON_CONS	20	21
FT	NON_CONS	28	29
FT	NON_TER	33	33

SQ SEQUENCE 33 AA; 3660 MW; 5BA16CC2880B7819 CRC64;

Query Match 14.7%; Score 5; DB 1; Length 33;
 Best Local Similarity 100.0%; Pred. No. 39;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEI 5
 |||||
 Db 13 SVSEI 17

RESULT 2

DMD_RAT

ID DMD_RAT STANDARD; PRT; 29 AA.
 AC P11530;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Dystrophin (Fragment).
 GN DMD.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88122671; PubMed=3340214;
 RA Nudel U., Robzyk K., Yaffe D.;
 RT "Expression of the putative Duchenne muscular dystrophy gene in
 RT differentiated myogenic cell cultures and in the brain.";
 RL Nature 331:635-638 (1988).
 CC -!- FUNCTION: May play a role in anchoring the cytoskeleton to the
 CC plasma membrane.
 CC -!- SUBUNIT: Interacts with the syntrophins SNTA1, SNTB1, SNTB2, SNTG1
 CC and SNTG2 (By similarity).
 CC -----
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 CC -----
 DR EMBL; X07000; CAA30057.1; -.
 DR PIR; S01614; S01614.
 DR InterPro; IPR001589; Actbind_actnin.
 DR InterPro; IPR001202; WW_Rsp5_WWP.
 DR PROSITE; PS00019; ACTININ_1; PARTIAL.
 DR PROSITE; PS00020; ACTININ_2; PARTIAL.
 DR PROSITE; PS01159; WW_DOMAIN_1; PARTIAL.
 DR PROSITE; PS50020; WW_DOMAIN_2; PARTIAL.
 KW Structural protein; Actin-binding; Calcium-binding; Cytoskeleton;
 KW Repeat.
 FT NON_TER 1 1
 FT NON_TER 29 29
 SQ SEQUENCE 29 AA; 3289 MW; 8ECFB28A1A7ACAF0 CRC64;

Query Match 11.8%; Score 4; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 KLQD 30
|||
Db 12 KLQD 15

RESULT 3

SCK2_LEIQH

ID SCK2_LEIQH STANDARD; PRT; 37 AA.
AC P45628;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Charybdotoxin 2 (ChTX-Lq2) (Toxin 18-2) (Lqh 18-2).
OS Leiurus quinquestriatus hebraeus (Yellow scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Buthoidea; Buthidae; Leiurus.
OX NCBI_TaxID=6884;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=90012179; PubMed=2477548;
RA Lucchesi K., Ravindran A., Young H., Moczydlowski E.;
RT "Analysis of the blocking activity of charybdotoxin homologs and
RT iodinated derivatives against Ca²⁺-activated K⁺ channels.";
RL J. Membr. Biol. 109:269-281(1989).
RN [2]
RP SEQUENCE OF 6-37.
RC TISSUE=Venom;
RX MEDLINE=95192968; PubMed=7533951;
RA Marshall D.L., Vatanpour H., Harvey A.L., Boyot P., Pinkasfeld S.,
RA Doljansky Y., Bouet F., Menez A.;
RT "Neuromuscular effects of some potassium channel blocking toxins from
RT the venom of the scorpion Leiurus quinquestriatus hebraeus.";
RL Toxicon 32:1433-1443(1994).
RN [3]
RP STRUCTURE BY NMR.
RX MEDLINE=99179991; PubMed=10081954;
RA Renisio J.G., Lu Z., Blanc E., Jin W., Lewis J.H., Bornet O.,
RA Darbon H.;
RT "Solution structure of potassium channel-inhibiting scorpion toxin
RT Lq2.";
RL Proteins 34:417-426(1999).
CC -!- FUNCTION: Has a potent presynaptic facilitatory action, with
CC less effect on direct muscle stimulation. Blocks calcium-
CC activated potassium channels.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -!- SIMILARITY: BELONGS TO THE SHORT SCORPION TOXIN FAMILY. POTASSIUM
CC CHANNEL INHIBITORS SUBFAMILY.
DR PIR; B60963; B60963.
DR PDB; 1LIR; 17-JUN-98.
DR InterPro; IPR001947; Scorpion_toxinS.
DR Pfam; PF00451; toxin_2; 1.

DR ProDom; PD003586; Scorpion_toxinS; 1.
 DR PROSITE; PS01138; SCORP_SHORT_TOXIN; 1.
 KW Toxin; Neurotoxin; Ionic channel inhibitor;
 KW Potassium channel inhibitor; Pyrrolidone carboxylic acid;
 KW 3D-structure.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT DISULFID 7 28
 FT DISULFID 13 33
 FT DISULFID 17 35
 FT SITE 26 33 INTERACTION WITH CA(2+)-ACTIVATED K(+)
 FT CHANNELS (POTENTIAL).
 FT HELIX 10 21
 FT STRAND 26 29
 FT TURN 30 31
 FT STRAND 32 35
 SQ SEQUENCE 37 AA; 4359 MW; 2D17819962644E32 CRC64;

Query Match 11.8%; Score 4; DB 1; Length 37;
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NR GK 13
 ||||
 Db 24 NR GK 27

RESULT 4

PSBY_SYNY3

ID PSBY_SYNY3 STANDARD; PRT; 39 AA.
 AC P73676;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Photosystem II protein Y.
 GN PSBY OR SML0007.
 OS Synechocystis sp. (strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
 OX NCBI_TaxID=1148;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97061201; PubMed=8905231;
 RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
 RA Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
 RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
 RA Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
 RA Tabata S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
 RT entire genome and assignment of potential protein-coding regions."
 RL DNA Res. 3:109-136(1996).
 CC !- FUNCTION: MANGANESE-BINDING POLYPEPTIDE WITH L-ARGININE
 CC METABOLIZING ENZYME ACTIVITY. COMPONENT OF THE CORE OF PHOTOSYSTEM
 CC II (BY SIMILARITY).
 CC !- SUBCELLULAR LOCATION: CELLULAR THYLAKOID MEMBRANE.
 CC !- SIMILARITY: BELONGS TO THE PSBY FAMILY.
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DR EMBL; D90908; BAA17722.1; -.

DR PIR; S77164; S77164.

KW Photosystem II; Transmembrane; Thylakoid; Complete proteome..

FT TRANSMEM 5 25 POTENTIAL.

SQ SEQUENCE 39 AA; 4202 MW; 3EA176ABAA79F6DF CRC64;

Query Match 11.8%; Score 4; DB 1; Length 39;

Best Local Similarity 100.0%; Pred. No. 5.4e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 LQDV 31

||||

Db 31 LQDV 34

RESULT 5

SR1C_SARPE

ID SR1C_SARPE STANDARD; PRT; 39 AA.

AC P08377;

DT 01-AUG-1988 (Rel. 08, Created)

DT 01-AUG-1988 (Rel. 08, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Sarcotoxin IC.

OS Sarcophaga peregrina (Flesh fly) (Boettcherisca peregrina).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;

OC Sarcophagidae; Sarcophaga.

OX NCBI_TaxID=7386;

RN [1]

RP SEQUENCE.

RX MEDLINE=85207747; PubMed=3888997;

RA Okada M., Natori S.;

RT "Primary structure of sarcotoxin I, an antibacterial protein induced

RT in the hemolymph of Sarcophaga peregrina (flesh fly) larvae.";

RL J. Biol. Chem. 260:7174-7177(1985).

CC -!- FUNCTION: SARCOTOXINS, WHICH ARE POTENT BACTERICIDAL PROTEINS,

CC ARE PRODUCED IN RESPONSE TO INJURY. THEY ARE CYTOTOXIC TO BOTH

CC GRAM-POSITIVE AND GRAM-NEGATIVE BACTERIA.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: BELONGS TO THE CECROPIN FAMILY.

DR PIR; C22625; CKFHCS.

DR InterPro; IPR000875; Cecropin.

DR InterPro; IPR003253; Sarctxn_cecrpn.

DR Pfam; PF00272; cecropin; 1.

DR ProDom; PD001670; Sarctxn_cecrpn; 1.

DR PROSITE; PS00268; CECROPIN; 1.

KW Insect immunity; Antibiotic; Hemolymph; Amidation; Multigene family.

FT MOD_RES 39 39 AMIDATION.

SQ SEQUENCE 39 AA; 4227 MW; 11E79F4F405E855A CRC64;

Query Match 11.8%; Score 4; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 WLRK 26
|||
Db 2 WLRK 5

RESULT 6

CH60_MYCSM

ID CH60_MYCSM STANDARD; PRT; 28 AA.
AC P80673;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 60 kDa chaperonin (Protein Cpn60) (groEL protein) (Fragment).
GN GROL OR GROEL OR MOPA.
OS Mycobacterium smegmatis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1772;
RN [1]
RP SEQUENCE.
RC STRAIN=ATCC 607 / mc(2)6 / NRRL B-692;
RX MEDLINE=97387814; PubMed=9243799;
RA Lundrigan M.D., Arceneaux J.E.L., Zhu W., Byers B.R.;
RT "Enhanced hydrogen peroxide sensitivity and altered stress protein
RT expression in iron-starved Mycobacterium smegmatis.";
RL BioMetals 10:215-225(1997).
CC -!- FUNCTION: Prevents misfolding and promotes the refolding and
CC proper assembly of unfolded polypeptides generated under stress
CC conditions.
CC -!- SUBUNIT: Oligomer of 14 subunits composed of two stacked rings of
CC 7 subunits (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the chaperonin (HSP60) family.
DR HAMAP; MF_00600; -; 1.
DR InterPro; IPR001844; Chaprnin_Cpn60.
DR PROSITE; PS00296; CHAPERONINS_CPN60; PARTIAL.
KW Chaperone; ATP-binding.
FT NON_TER 28 28
SQ SEQUENCE 28 AA; 3047 MW; 2F40F27B94EF8720 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
|||
Db 18 LNS 20

RESULT 7

COXB_SOLTU

ID COXB_SOLTU STANDARD; PRT; 28 AA.
AC P80499;

DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Cytochrome c oxidase polypeptide Vb (EC 1.9.3.1) (Fragment).
 OS Solanum tuberosum (Potato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamiids; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4113;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Tuber;
 RX MEDLINE=97077345; PubMed=8919912;
 RA Jansch L., Krufft V., Schmitz U.K., Braun H.P.;
 RT "New insights into the composition, molecular mass and stoichiometry
 RT of the protein complexes of plant mitochondria.";
 RL Plant J. 9:357-368(1996).
 CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
 CC c + 2 H(2)O.
 CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
 CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VB FAMILY.
 DR InterPro; IPR002124; COX5B.
 DR PROSITE; PS00848; COX5B; PARTIAL.
 KW Oxidoreductase; Inner membrane; Mitochondrion.
 FT NON_TER 28 28
 SQ SEQUENCE 28 AA; 3101 MW; 1EAFA79E2682849C CRC64;

Query Match 8.8%; Score 3; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 4.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSE 4
 |||
 Db 2 VSE 4

RESULT 8

GUN_SCHCO

ID GUN_SCHCO STANDARD; PRT; 28 AA.
 AC P81190;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Endoglucanase (EC 3.2.1.4) (Endo-1,4-beta-glucanase) (Cellulase)
 DE (Fragment).
 OS Schizophyllum commune (Bracket fungus).
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
 OC Agaricales; Schizophyllaceae; Schizophyllum.
 OX NCBI_TaxID=5334;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=97459758; PubMed=9315718;
 RA Clarke A.J., Drummelsmith J., Yaguchi M.;
 RT "Identification of the catalytic nucleophile in the cellulase from
 RT Schizophyllum commune and assignment of the enzyme to Family 5,
 RT subtype 5 of the glycosidases.";
 RL FEBS Lett. 414:359-361(1997).

CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic
 CC linkages in cellulose, lichenin and cereal beta-D-glucans.
 CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
 CC (Probable).
 CC -!- SIMILARITY: BELONGS TO CELLULASE FAMILY A (FAMILY 5 OF GLYCOSYL
 CC HYDROLASES).
 DR InterPro; IPR001547; Glyco_hydro_5.
 DR PROSITE; PS00659; GLYCOSYL_HYDROL_F5; PARTIAL.
 KW Cellulose degradation; Hydrolase; Glycosidase; Zymogen; Membrane;
 KW Lipoprotein.
 FT ACT_SITE 20 20 NUCLEOPHILE.
 FT NON_TER 28 28
 SQ SEQUENCE 28 AA; 2937 MW; B3F1C0C99C9950BE CRC64;

Query Match. 8.8%; Score 3; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 4.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 EWL 24
 |||
 Db 7 EWL 9

RESULT 9

PA2C_PSEPO

ID PA2C_PSEPO STANDARD; PRT; 28 AA.
 AC P20260;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Phospholipase A2 (EC 3.1.1.4) (Pseudexin C chain) (Phosphatidylcholine
 DE 2-acylhydrolase) (Fragment).
 OS Pseudechis porphyriacus (Red-bellied black snake).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Acanthophiinae; Pseudechis.
 OX NCBI_TaxID=8671;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=89388835; PubMed=2675391;
 RA Schmidt J.J., Middlebrook J.L.;
 RT "Purification, sequencing and characterization of pseudexin
 RT phospholipases A2 from Pseudechis porphyriacus (Australian
 RT red-bellied black snake).";
 RL Toxicon 27:805-818(1989).
 CC -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-
 CC acyl groups in 3-sn-phosphoglycerides.
 CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
 CC acylglycerophosphocholine + a fatty acid anion.
 CC -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY. GROUP I
 CC SUBFAMILY.
 DR PIR; C32416; C32416.
 DR HSSP; P00592; 2PHI.
 DR InterPro; IPR001211; PhospholipaseA2.

DR Pfam; PF00068; phoslip; 1.
 DR ProDom; PD000303; PhospholipaseA2; 1.
 DR PROSITE; PS00119; PA2_ASP; PARTIAL.
 DR PROSITE; PS00118; PA2_HIS; PARTIAL.
 KW Hydrolase; Lipid degradation; Calcium; Multigene family.
 FT NON_TER 28 28
 SQ SEQUENCE 28 AA; 3210 MW; 5089A7E85CAAE0D5 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 4.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 IQL 7
 |||
 Db 3 IQL 5

RESULT 10

VIP_ALLMI

ID VIP_ALLMI STANDARD; PRT; 28 AA.
 AC P48142; P01285;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Vasoactive intestinal peptide (VIP).
 GN VIP.
 OS Alligator mississippiensis (American alligator).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Crocodylidae; Alligatorinae; Alligator.
 OX NCBI_TaxID=8496;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Stomach;
 RX MEDLINE=93324451; PubMed=8101369;
 RA Wang Y., Conlon J.M.;
 RT "Neuroendocrine peptides (NPY, GRP, VIP, somatostatin) from the brain
 RT and stomach of the alligator."
 RL Peptides 14:573-579(1993).
 CC -!- FUNCTION: VIP CAUSES VASODILATION, LOWERS ARTERIAL BLOOD
 CC PRESSURE, STIMULATES MYOCARDIAL CONTRACTILITY, INCREASES
 CC GLYCOGENOLYSIS AND RELAXES THE SMOOTH MUSCLE OF TRACHEA, STOMACH
 CC AND GALL BLADDER.
 CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
 DR InterPro; IPR000532; Glucagon.
 DR Pfam; PF00123; hormone2; 1.
 DR PRINTS; PR00275; GLUCAGON.
 DR SMART; SM00070; GLUCA; 1.
 DR PROSITE; PS00260; GLUCAGON; 1.
 KW Glucagon family; Amidation; Hormone.
 FT MOD_RES 28 28 AMIDATION.
 SQ SEQUENCE 28 AA; 3320 MW; 17B42D7573FF6F37 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 4.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17

Db |||
 23 LNS 25

RESULT 11

VIP_RANRI

ID VIP_RANRI STANDARD; PRT; 28 AA.
AC P81016;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Vasoactive intestinal peptide (VIP).
OS Rana ridibunda (Laughing frog) (Marsh frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8406;
RN [1]
RP SEQUENCE.
RX MEDLINE=95309202; PubMed=7540547;
RA Chartrel N., Wang Y., Fournier A., Vaudry H., Conlon J.M.;
RT "Frog vasoactive intestinal polypeptide and galanin: primary
RT structures and effects on pituitary adenylate cyclase."
RL Endocrinology 136:3079-3086(1995).
CC -!- FUNCTION: VIP CAUSES VASODILATION, LOWERS ARTERIAL BLOOD
CC PRESSURE, STIMULATES MYOCARDIAL CONTRACTILITY, INCREASES
CC GLYCOGENOLYSIS AND RELAXES THE SMOOTH MUSCLE OF TRACHEA, STOMACH
CC AND GALL BLADDER.
CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
DR InterPro; IPR000532; Glucagon.
DR Pfam; PF00123; hormone2; 1.
DR PRINTS; PR00275; GLUCAGON.
DR PROSITE; PS00260; GLUCAGON; 1.
KW Glucagon family; Amidation; Hormone.
FT MOD_RES 28 28 AMIDATION.
SQ SEQUENCE 28 AA; 3320 MW; 17B42D7573FF6F37 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
 |||
Db 23 LNS 25

RESULT 12

VIP_SHEEP

ID VIP_SHEEP STANDARD; PRT; 28 AA.
AC P04565;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Vasoactive intestinal peptide (VIP).
GN VIP.
OS Ovis aries (Sheep),
OS Capra hircus (Goat), and
OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940, 9925, 9615;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=Sheep; TISSUE=Brain;
 RX MEDLINE=91045331; PubMed=2235680;
 RA Gafvelin G.;
 RT "Isolation and primary structure of VIP from sheep brain.";
 RL Peptides 11:703-706(1990).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=Sheep; TISSUE=Small intestine;
 RX MEDLINE=91239834; PubMed=2034821;
 RA Bounjoua Y., Vandermeers A., Robberecht P., Vandermeers-Piret M.C.,
 RA Christophe J.;
 RT "Purification and amino acid sequence of vasoactive intestinal
 RT peptide, peptide histidine isoleucinamide and secretin from the ovine
 RT small intestine.";
 RL Regul. Pept. 32:169-179(1991).
 RN [3]
 RP SEQUENCE.
 RC SPECIES=C.hircus, and C.familiaris;
 RX MEDLINE=86313167; PubMed=3748846;
 RA Eng J., Du B.-H., Raufman J.-P., Yalow R.S.;
 RT "Purification and amino acid sequences of dog, goat and guinea pig
 RT VIPs.";
 RL Peptides 7 Suppl. 1:17-20(1986).
 CC -!- FUNCTION: VIP CAUSES VASODILATION, LOWERS ARTERIAL BLOOD
 CC PRESSURE, STIMULATES MYOCARDIAL CONTRACTILITY, INCREASES
 CC GLYCOGENOLYSIS AND RELAXES THE SMOOTH MUSCLE OF TRACHEA, STOMACH
 CC AND GALL BLADDER.
 CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
 DR PIR; A60304; A60304.
 DR PIR; B60072; VRSH.
 DR InterPro; IPR000532; Glucagon.
 DR Pfam; PF00123; hormone2; 1.
 DR PRINTS; PR00275; GLUCAGON.
 DR SMART; SM00070; GLUCA; 1.
 DR PROSITE; PS00260; GLUCAGON; 1.
 KW Glucagon family; Amidation; Hormone.
 FT MOD_RES 28 28 AMIDATION.
 SQ SEQUENCE 28 AA; 3327 MW; EF313FB573FF6F3F CRC64;

Query Match 8.8%; Score 3; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 4.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LNS 17
 |||
 Db 23 LNS 25

RESULT 13
 CXOC_CONMA
 ID CXOC_CONMA STANDARD; PRT; 29 AA.

AC P37300;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Omega-conotoxin MVIIC precursor (SNX-230) (Fragment).
 OS Conus magus (Magus cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=6492;
 RN [1]
 RP SEQUENCE FROM N.A., AND SYNTHESIS.
 RX MEDLINE=92337922; PubMed=1352986;
 RA Hillyard D.R., Monje V.D., Mintz I.M., Bean B.P., Nadasdi L.,
 RA Ramachandran J., Miljanich G.P., Azimi-Zoonooz A., McIntosh J.M.,
 RA Cruz L.J., Imperial J.S., Olivera B.M.;
 RT "A new Conus peptide ligand for mammalian presynaptic Ca²⁺ channels.";
 RL Neuron 9:69-77(1992).
 RN [2]
 RP STRUCTURE BY NMR.
 RX MEDLINE=95248539; PubMed=7731037;
 RA Farr-Jones S., Miljanich G.P., Nadasdi L., Ramachandran J.,
 RA Basus V.J.;
 RT "Solution structure of omega-conotoxin MVIIC, a high affinity ligand
 RT of P-type calcium channels, using 1H NMR spectroscopy and complete
 RT relaxation matrix analysis.";
 RL J. Mol. Biol. 248:106-124(1995).
 RN [3]
 RP STRUCTURE BY NMR.
 RX MEDLINE=99303703; PubMed=10373375;
 RA Nielsen K.J., Adams D., Thomas L., Bond T., Alewood P.F., Craik D.J.,
 RA Lewis R.J.;
 RT "Structure-activity relationships of omega-conotoxins MVIIA, MVIIC and
 RT 14 loop splice hybrids at N and P/Q-type calcium channels.";
 RL J. Mol. Biol. 289:1405-1421(1999).
 RN [4]
 RP MUTAGENESIS OF TYR-15.
 RX MEDLINE=95408251; PubMed=7677735;
 RA Kim J.I., Takahashi M., Martin-Moutot N., Seagar M.J., Ohtake A.,
 RA Sato K.;
 RT "Tyr13 is essential for the binding of omega-conotoxin MVIIC to the
 RT P/Q-type calcium channel.";
 RL Biochem. Biophys. Res. Commun. 214:305-309(1995).
 CC -!- FUNCTION: Omega-conotoxins act at presynaptic membranes, they bind
 CC and block voltage-sensitive calcium channels (VSCC). This toxin
 CC blocks N-type calcium channels as well as types of high-threshold
 CC voltage-gated calcium channels resistant to both dihydropyridines
 CC and omega-conotoxin GVIA.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -!- SIMILARITY: BELONGS TO THE O-SUPERFAMILY OF CONOTOXINS. OMEGA-TYPE
 CC FAMILY.
 CC -----
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DR EMBL; S40826; AAB22674.1; -.

DR PIR; JH0699; JH0699.

DR PDB; 1OMN; 01-DEC-95.

DR PDB; 1CNN; 31-MAY-00.

KW Toxin; Neurotoxin; Presynaptic neurotoxin; Ionic channel inhibitor;

KW Calcium channel inhibitor; Hydroxylation; Amidation; 3D-structure.

FT NON_TER 1 1

FT PROPEP <1 2

FT PEPTIDE 3 28 OMEGA-CONOTOXIN MVIIC.

FT BINDING 15 15 ESSENTIAL FOR CALCIUM CHANNEL BINDING.

FT DISULFID 3 18

FT DISULFID 10 22

FT DISULFID 17 28

FT MOD_RES 9 9 HYDROXYLATION (PROBABLE).

FT MOD_RES 28 28 AMIDATION (G-29 PROVIDE AMIDE GROUP).

FT MUTAGEN 15 15 Y->A: HIGH DECREASE IN BINDING.

FT TURN 6 7

FT STRAND 9 9

FT HELIX 12 14

FT TURN 24 25

FT STRAND 27 27

SQ SEQUENCE 29 AA; 3071 MW; AC7A68948474728A CRC64;

Query Match 8.8%; Score 3; DB 1; Length 29;

Best Local Similarity 100.0%; Pred. No. 4.8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RGK 13

|||

Db 25 RGK 27

RESULT 14

CXOD_CONMA

ID CXOD_CONMA STANDARD; PRT; 29 AA.

AC Q26350;

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Omega-conotoxin MVIId precursor (SNX-238) (Fragment).

OS Conus magus (Magus cone).

OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;

OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;

OC Neogastropoda; Conoidea; Conidae; Conus.

OX NCBI_TaxID=6492;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=94150815; PubMed=8107968;

RA Monje V.D., Haack J.A., Naisbitt S.R., Miljanich G., Ramachandran J.,

RA Nasdasdi L., Olivera B.M., Hillyard D.R., Gray W.R.;

RT "A new Conus peptide ligand for Ca channel subtypes.";

RL Neuropharmacology 32:1141-1149(1993).

RN [2]

RP STRUCTURE BY NMR.
RX MEDLINE=99121185; PubMed=9920728;
RA Civera C., Vazquez A., Sevilla J.M., Bruix M., Gago F., Garcia A.G.,
RA Sevilla P.;
RT "Solution structure determination by two-dimensional 1H NMR of
RT omega-conotoxin MVIID, a calcium channel blocker peptide.";
RL Biochem. Biophys. Res. Commun. 254:32-35(1999).
CC -!- FUNCTION: Omega-conotoxins act at presynaptic membranes, they bind
CC and block voltage-sensitive calcium channels (VSCC). This toxin
CC blocks channels of the N-type as well as other types.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- SIMILARITY: BELONGS TO THE O-SUPERFAMILY OF CONOTOXINS. OMEGA-TYPE
CC FAMILY.
CC -----
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CC -----
DR EMBL; S69322; AAB29902.1; -.
DR PIR; A58537; A58537.
DR HSSP; P05484; 1MVI.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
KW Toxin; Neurotoxin; Presynaptic neurotoxin; Ionic channel inhibitor;
KW Calcium channel inhibitor; Amidation.
FT NON_TER 1 1
FT PROPEP <1 3
FT PEPTIDE 4 28 OMEGA-CONOTOXIN MVIID.
FT DISULFID 4 19
FT DISULFID 11 23
FT DISULFID 18 28
FT MOD_RES 28 28 AMIDATION (G-29 PROVIDE AMIDE GROUP).
SQ SEQUENCE 29 AA; 3104 MW; 9E04B2EA3779CB22 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NRG 12
|||
Db 24 NRG 26

RESULT 15

GALA_ALLMI
ID GALA_ALLMI STANDARD; PRT; 29 AA.
AC P47215;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Galanin.
OS Alligator mississippiensis (American alligator).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Crocodylidae; Alligatorinae; Alligator.
 OX NCBI_TaxID=8496;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Stomach;
 RX MEDLINE=95023390; PubMed=7524049;
 RA Wang Y., Conlon J.M.;
 RT "Purification and primary structure of galanin from the alligator
 RT stomach.";
 RL Peptides 15:603-606(1994).
 CC -!- FUNCTION: CONTRACTS SMOOTH MUSCLE OF THE GASTROINTESTINAL AND
 CC GENITOURINARY TRACT, REGULATES GROWTH HORMONE RELEASE, MODULATES
 CC INSULIN RELEASE, AND MAY BE INVOLVED IN THE CONTROL OF ADRENAL
 CC SECRETION.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE GALANIN FAMILY.
 DR InterPro; IPR001600; Galanin.
 DR Pfam; PF01296; Galanin; 1.
 DR ProDom; PD005962; Galanin; 1.
 DR PROSITE; PS00861; GALANIN; 1.
 KW Hormone; Neuropeptide; Amidation.
 FT MOD_RES 29 29 AMIDATION.
 SQ SEQUENCE 29 AA; 3216 MW; E02F019B2D3E0529 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 4.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
 |||
 Db 4 LNS 6

RESULT 16

GALA_AMICA

ID GALA_AMICA STANDARD; PRT; 29 AA.
 AC P47214;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Galanin.
 OS Amia calva (Bowfin).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Amiiformes; Amiidae; Amia.
 OX NCBI_TaxID=7924;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Stomach;
 RX MEDLINE=95083480; PubMed=7527531;
 RA Wang Y., Conlon J.M.;
 RT "Purification and characterization of galanin from the
 RT phylogenetically ancient fish, the bowfin (*Amia calva*) and dogfish
 RT (*Scyliorhinus canicula*).";
 RL Peptides 15:981-986(1994).
 CC -!- FUNCTION: CONTRACTS SMOOTH MUSCLE OF THE GASTROINTESTINAL AND
 CC GENITOURINARY TRACT, REGULATES GROWTH HORMONE RELEASE, MODULATES

CC INSULIN RELEASE, AND MAY BE INVOLVED IN THE CONTROL OF ADRENAL
 CC SECRETION.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE GALANIN FAMILY.
 DR InterPro; IPR001600; Galanin.
 DR Pfam; PF01296; Galanin; 1.
 DR ProDom; PD005962; Galanin; 1.
 DR PROSITE; PS00861; GALANIN; 1.
 KW Hormone; Neuropeptide; Amidation.
 FT MOD_RES 29 29 AMIDATION.
 SQ SEQUENCE 29 AA; 3114 MW; 7518719B2D271627 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 4.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
 |||
 Db 4 LNS 6

RESULT 17

GALA_CHICK

ID GALA_CHICK STANDARD; PRT; 29 AA.
 AC P30802;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Galanin.
 GN GAL OR GALN.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Intestine;
 RX MEDLINE=91348254; PubMed=1715289;
 RA Norberg A., Sillard R., Carlquist M., Joernvall H., Mutt V.;
 RT "Chemical detection of natural peptides by specific structures.
 RT Isolation of chicken galanin by monitoring for its N-terminal
 RT dipeptide, and determination of the amino acid sequence.";
 RL FEBS Lett. 288:151-153(1991).
 CC -!- FUNCTION: CONTRACTS SMOOTH MUSCLE OF THE GASTROINTESTINAL AND
 CC GENITOURINARY TRACT, REGULATES GROWTH HORMONE RELEASE, MODULATES
 CC INSULIN RELEASE, AND MAY BE INVOLVED IN THE CONTROL OF ADRENAL
 CC SECRETION.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE GALANIN FAMILY.
 DR PIR; S17147; S17147.
 DR InterPro; IPR001600; Galanin.
 DR Pfam; PF01296; Galanin; 1.
 DR PRINTS; PR00273; GALANIN.
 DR ProDom; PD005962; Galanin; 1.
 DR PROSITE; PS00861; GALANIN; 1.
 KW Hormone; Neuropeptide; Amidation.

FT MOD_RES 29 29 AMIDATION.
SQ SEQUENCE 29 AA; 3212 MW; EB66919B2D271629 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
|||
Db 4 LNS 6

RESULT 18

GALA_ONCMY

ID GALA_ONCMY STANDARD; PRT; 29 AA.
AC P47213;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Galanin.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE.
RC TISSUE=Stomach;
RX MEDLINE=95164756; PubMed=7532194;
RA Anglade I., Wang Y., Jensen J., Tramu G., Kah O., Conlon J.M.;
RT "Characterization of trout galanin and its distribution in trout
RT brain and pituitary.";
RL J. Comp. Neurol. 350:63-74(1994).
CC -!- FUNCTION: CONTRACTS SMOOTH MUSCLE OF THE GASTROINTESTINAL AND
CC GENITOURINARY TRACT, REGULATES GROWTH HORMONE RELEASE, MODULATES
CC INSULIN RELEASE, AND MAY BE INVOLVED IN THE CONTROL OF ADRENAL
CC SECRETION.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE GALANIN FAMILY.
DR InterPro; IPR001600; Galanin.
DR Pfam; PF01296; Galanin; 1.
DR ProDom; PD005962; Galanin; 1.
DR PROSITE; PS00861; GALANIN; 1.
KW Hormone; Neuropeptide; Amidation.
FT MOD_RES 29 29 AMIDATION.
SQ SEQUENCE 29 AA; 3044 MW; 73C37190403FA349 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
|||
Db 4 LNS 6

RESULT 19

GALA_RANRI

ID GALA_RANRI STANDARD; PRT; 29 AA.
 AC P47216;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Galanin.
 OS Rana ridibunda (Laughing frog) (Marsh frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
 OX NCBI_TaxID=8406;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95309202; PubMed=7540547;
 RA Chartrel N., Wang Y., Fournier A., Vaudry H., Conlon J.M.;
 RT "Frog vasoactive intestinal polypeptide and galanin: primary
 RT structures and effects on pituitary adenylate cyclase."
 RL Endocrinology 136:3079-3086(1995).
 CC -!- FUNCTION: CONTRACTS SMOOTH MUSCLE OF THE GASTROINTESTINAL AND
 CC GENITOURINARY TRACT, REGULATES GROWTH HORMONE RELEASE, MODULATES
 CC INSULIN RELEASE, AND MAY BE INVOLVED IN THE CONTROL OF ADRENAL
 CC SECRETION.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE GALANIN FAMILY.
 DR InterPro; IPR001600; Galanin.
 DR Pfam; PF01296; Galanin; 1.
 DR ProDom; PD005962; Galanin; 1.
 DR PROSITE; PS00861; GALANIN; 1.
 KW Hormone; Neuropeptide; Amidation.
 FT MOD_RES 29 29 AMIDATION.
 SQ SEQUENCE 29 AA; 3162 MW; F718719B2D3FB529 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 4.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LNS 17
 |||
 Db 4 LNS 6

RESULT 20

GALA_SHEEP

ID GALA_SHEEP STANDARD; PRT; 29 AA.
 AC P31234;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Galanin.
 GN GAL OR GALN OR GLNN.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE.

RC TISSUE=Brain;
 RX MEDLINE=92158824; PubMed=1724081;
 RA Sillard R., Langel U., Joernvall H.;
 RT "Isolation and characterization of galanin from sheep brain.";
 RL Peptides 12:855-859(1991).
 CC -!- FUNCTION: CONTRACTS SMOOTH MUSCLE OF THE GASTROINTESTINAL AND
 CC GENITOURINARY TRACT, REGULATES GROWTH HORMONE RELEASE, MODULATES
 CC INSULIN RELEASE, AND MAY BE INVOLVED IN THE CONTROL OF ADRENAL
 CC SECRETION.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE GALANIN FAMILY.
 DR InterPro; IPR001600; Galanin.
 DR Pfam; PF01296; Galanin; 1.
 DR PRINTS; PR00273; GALANIN.
 DR ProDom; PD005962; Galanin; 1.
 DR PROSITE; PS00861; GALANIN; 1.
 KW Hormone; Neuropeptide; Amidation.
 FT MOD_RES 29 29 AMIDATION.
 SQ SEQUENCE 29 AA; 3185 MW; F718719B2D3FB089 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 4.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LNS 17
 |||
 Db 4 LNS 6

RESULT 21

GLUC_CHIBR

ID GLUC_CHIBR STANDARD; PRT; 29 AA.
 AC P31297;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Glucagon.
 GN GCG.
 OS Chinchilla brevicaudata (Chinchilla).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Chinchillidae;
 OC Chinchilla.
 OX NCBI_TaxID=10152;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=91045327; PubMed=2235678;
 RA Eng J., Kleinman W.A., Chu L.S.;
 RT "Purification of peptide hormones from chinchilla pancreas by
 RT chemical assay.";
 RL Peptides 11:683-685(1990).
 CC -!- FUNCTION: PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPIDS, AND RAISES
 CC THE BLOOD SUGAR LEVEL.
 CC -!- INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS
 CC IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.
 CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
 DR PIR; A60413; GCCB.
 DR HSSP; P01275; 1BH0.

DR InterPro; IPR000532; Glucagon.
 DR Pfam; PF00123; hormone2; 1.
 DR PRINTS; PR00275; GLUCAGON.
 DR SMART; SM00070; GLUCA; 1.
 DR PROSITE; PS00260; GLUCAGON; 1.
 KW Glucagon family; Hormone.
 SQ SEQUENCE 29 AA; 3478 MW; 19ECF4DABB752B27 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 4.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 KHL 15
 |||
 Db 12 KHL 14

RESULT 22

IPYR_DESVH

ID IPYR_DESVH STANDARD; PRT; 29 AA.
 AC P19371;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Inorganic pyrophosphatase (EC 3.6.1.1) (Pyrophosphate phospho-
 DE hydrolase) (PPase) (Fragment).
 OS Desulfovibrio vulgaris (strain Hildenborough).
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;
 OC Desulfovibrionaceae; Desulfovibrio.
 OX NCBI_TaxID=882;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=90365722; PubMed=2168174;
 RA Liu M.-Y., le Gall J.;
 RT "Purification and characterization of two proteins with inorganic
 RT pyrophosphatase activity from Desulfovibrio vulgaris: rubrerythrin
 RT and a new, highly active, enzyme."
 RL Biochem. Biophys. Res. Commun. 171:313-318(1990).
 CC -!- FUNCTION: INORGANIC PYROPHOSPHATASE IS AN ESSENTIAL ENZYME FOR THE
 CC ACTIVATION OF SULFATE BY SULFATE REDUCING BACTERIA. THIS IS A HIGH
 CC ACTIVITY PYROPHOSPHATASE.
 CC -!- CATALYTIC ACTIVITY: Diphosphate + H(2)O = 2 phosphate.
 CC -!- SUBCELLULAR LOCATION: Periplasmic (Potential).
 DR PIR; A35687; A35687.
 DR HAMAP; MF_00209; -; 1.
 DR InterPro; IPR001596; Pyrophosphatase.
 DR PROSITE; PS00387; PPASE; PARTIAL.
 KW Hydrolase; Periplasmic.
 FT NON_TER 29 29
 SQ SEQUENCE 29 AA; 3201 MW; 3FC5792360F2227B CRC64;

Query Match 8.8%; Score 3; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 4.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SEI 5
 |||

Db

15 SEI 17

RESULT 23

NUO1_SOLTU

ID NUO1_SOLTU STANDARD; PRT; 29 AA.
AC P80267;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE NADH-ubiquinone oxidoreductase 14 kDa subunit (EC 1.6.5.3)
DE (EC 1.6.99.3) (Complex I-14KD) (CI-14KD) (Fragment).
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamiids; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. Bintje; TISSUE=Tuber;
RX MEDLINE=94124587; PubMed=8294484;
RA Herz U., Schroeder W., Liddell A., Leaver C.J., Brennicke A.,
RA Grohmann L.;
RT "Purification of the NADH:ubiquinone oxidoreductase (complex I) of
RT the respiratory chain from the inner mitochondrial membrane of
RT Solanum tuberosum.";
RL J. Biol. Chem. 269:2263-2269(1994).
CC -!- FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY
CC CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED
CC TO BE UBIQUINONE.
CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -!- CATALYTIC ACTIVITY: NADH + acceptor = NAD(+) + reduced acceptor.
CC -!- SUBUNIT: COMPLEX I IS COMPOSED OF ABOUT 30 DIFFERENT SUBUNITS.
CC -!- SUBCELLULAR LOCATION: MATRIX SIDE OF THE MITOCHONDRIAL INNER
CC MEMBRANE.
DR PIR; I49732; I49732.
KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
FT NON_TER 29 29
SQ SEQUENCE 29 AA; 3269 MW; E2B4DFB558D423D4 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 25 RKK 27
|||
Db 2 RKK 4

RESULT 24

PCG4_PACGO

ID PCG4_PACGO STANDARD; PRT; 29 AA.
AC P82417;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ponericin G4.

OS Pachycondyla goeldii (Ponerine ant).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Formicidae;
 OC Ponerinae; Pachycondyla.
 OX NCBI_TaxID=118888;
 RN [1]
 RP SEQUENCE, AND FUNCTION.
 RC TISSUE=Venom;
 RX MEDLINE=21264562; PubMed=11279030;
 RA Orivel J., Redeker V., Le Caer J.-P., Krier F., Revol-Junelles A.-M.,
 RA Longeon A., Chafotte A., Dejean A., Rossier J.;
 RT "Ponericins, new antibacterial and insecticidal peptides from the
 RT venom of the ant Pachycondyla goeldii.";
 RL J. Biol. Chem. 276:17823-17829(2001).
 CC -!- FUNCTION: HAS ACTIVITY AGAINST SOME GRAM-POSITIVE BACTERIA
 CC AND S.CEREVISIAE. HAS A NON-HEMOLYTIC ACTIVITY.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- MASS SPECTROMETRY: MW=3163.87; METHOD=MALDI.
 KW Antibiotic; Insect immunity; Fungicide.
 SQ SEQUENCE 29 AA; 3165 MW; 7037D0B855072AF8 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 4.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 EWL 24
 |||
 Db 11 EWL 13

RESULT 25

RS7_METTE

ID RS7_METTE STANDARD; PRT; 29 AA.
 AC O93639;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 30S ribosomal protein S7P (Fragment).
 GN RPS7P OR S7.
 OS Methanosarcina thermophila.
 OC Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;
 OC Methanosarcinales; Methanosarcinaceae; Methanosarcina.
 OX NCBI_TaxID=2210;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DSM 1825 / TM-1;
 RX MEDLINE=99059471; PubMed=9845338;
 RA Thomas T., Cavicchioli R.;
 RT "Archaeal cold-adapted proteins: structural and evolutionary analysis
 RT of the elongation factor 2 proteins from psychrophilic, mesophilic and
 RT thermophilic methanogens.";
 RL FEBS Lett. 439:281-287(1998).
 CC -!- FUNCTION: One of the primary rRNA binding proteins, it binds
 CC directly to 16S rRNA where it nucleates assembly of the head
 CC domain of the 30S subunit. Is located at the subunit interface
 CC close to the decoding center (By similarity).
 CC -!- SUBUNIT: Part of the 30S ribosomal subunit.

CC -!- SIMILARITY: BELONGS TO THE S7P FAMILY OF RIBOSOMAL PROTEINS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF026165; AAC79199.1; -.
 DR PIR; T44245; T44245.
 DR HAMAP; MF_00480; -; 1.
 DR InterPro; IPR000235; Ribosomal_S7.
 DR PROSITE; PS00052; RIBOSOMAL_S7; PARTIAL.
 KW Ribosomal protein; RNA-binding; rRNA-binding.
 FT NON_TER 1 1
 SQ SEQUENCE 29 AA; 3217 MW; 1602B8A2E6C50C2B CRC64;

Query Match 8.8%; Score 3; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 4.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 ERV 21
 |||
 Db 22 ERV 24

RESULT 26

SODC_OLEEU

ID SODC_OLEEU STANDARD; PRT; 29 AA.
 AC P80740;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Superoxide dismutase [Cu-Zn] (EC 1.15.1.1) (Allergen Ole e 5) (Ole e
 DE V) (Fragment).
 OS Olea europaea (Common olive).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamiids; Lamiales; Oleaceae; Olea.
 OX NCBI_TaxID=4146;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Pollen;
 RX MEDLINE=98160390; PubMed=9500754;
 RA Boluda L., Alonso C., Fernandez-Caldas E.;
 RT "Purification, characterization, and partial sequencing of two new
 RT allergens of Olea europaea."
 RL J. Allergy Clin. Immunol. 101:210-216(1998).
 CC -!- FUNCTION: Destroys radicals which are normally produced within the
 CC cells and which are toxic to biological systems (By similarity).
 CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
 CC -!- COFACTOR: Binds 1 copper ion and 1 zinc ion per subunit (By
 CC similarity).
 CC -!- SIMILARITY: BELONGS TO THE CU-ZN SUPEROXIDE DISMUTASE FAMILY.
 DR InterPro; IPR001424; SOD_CU_ZN.

DR Pfam; PF00080; sodcu; 1.
DR PROSITE; PS00087; SOD_CU_ZN_1; PARTIAL.
DR PROSITE; PS00332; SOD_CU_ZN_2; PARTIAL.
KW Antioxidant; Oxidoreductase; Metal-binding; Copper; Zinc; Allergen.
FT NON_TER 29 29
SQ SEQUENCE 29 AA; 2973 MW; 836C7A193EDAD71E CRC64;

Query Match 8.8%; Score 3; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
|||
Db 7 LNS 9

RESULT 27

TL16_SPIOL

ID TL16_SPIOL STANDARD; PRT; 29 AA.
AC P81834;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Thylakoid lumenal 16.5 kDa protein (P16.5) (Fragment).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE.
RC TISSUE=Leaf;
RX MEDLINE=98175931; PubMed=9506969;
RA Kieselbach T., Hagman A., Andersson B., Schroeder W.P.;
RT "The thylakoid lumen of chloroplasts. Isolation and
RT characterization.";
RL J. Biol. Chem. 273:6710-6716(1998).
CC -!- SUBCELLULAR LOCATION: Chloroplast; within the thylakoid lumen.
KW Chloroplast; Thylakoid.
FT NON_TER 29 29
SQ SEQUENCE 29 AA; 3464 MW; 58B785764E2623E3 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 25 RKK 27
|||
Db 19 RKK 21

RESULT 28

CX7A_CONTU

ID CX7A_CONTU STANDARD; PRT; 30 AA.
AC P58923;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Conotoxin TVIIA.
 OS Conus tulipa (Fish-hunting cone snail) (Tulip cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=6495;
 RN [1]
 RP SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND COMPARISON WITH CONOTOXIN
 RP GS.
 RC TISSUE=Venom;
 RX MEDLINE=20363693; PubMed=10903496;
 RA Hill J.M., Atkins A.R., Loughnan M.L., Jones A., Adams D.A.,
 RA Martin R.C., Lewis R.J., Craik D.J., Alewood P.F.;
 RT "Conotoxin TVIIA, a novel peptide from the venom of Conus tulipa 1.
 RT Isolation, characterization and chemical synthesis.";
 RL Eur. J. Biochem. 267:4642-4648(2000).
 RN [2]
 RP SYNTHESIS, STRUCTURE BY NMR, AND COMPARISON WITH CONOTOXIN GS.
 RX MEDLINE=20363694; PubMed=10903497;
 RA Hill J.M., Alewood P.F., Craik D.J.;
 RT "Conotoxin TVIIA, a novel peptide from the venom of Conus tulipa 2.
 RT Three-dimensional solution structure.";
 RL Eur. J. Biochem. 267:4649-4657(2000).
 CC -!- FUNCTION: By structural similarity with conotoxin GS, may inhibit
 CC the sodium channel. No effect was observed upon intracranial
 CC injections into mice and intraperitoneal injections into goldfish
 CC (25 microgrammes).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -!- PTM: Three different forms of TVIIA exist. Pro-10 and Pro-11 of
 CC conotoxin TVIIA are hydroxylated in TVIIA, whereas Pro-10 is not
 CC hydroxylated in [Pro10]TVIIA, and neither Pro-10 nor Pro-11 are
 CC hydroxylated in [Pro10,11]TVIIA.
 CC -!- MASS SPECTROMETRY: MW=3212.4; METHOD=Electrospray; RANGE=Isoform
 CC TVIIA.
 CC -!- MASS SPECTROMETRY: MW=3196.0; METHOD=Electrospray; RANGE=Isoform
 CC [Pro10]TVIIA.
 CC -!- MASS SPECTROMETRY: MW=3180.0; METHOD=Electrospray;
 CC RANGE=Isoform [Pro10,Pro11]TVIIA.
 CC -!- SIMILARITY: BELONGS TO THE O-SUPERFAMILY OF CONOTOXINS.
 DR PDB; 1EYO; 06-SEP-00.
 KW Toxin; Hydroxylation; 3D-structure.
 FT DISULFID 2 14
 FT DISULFID 9 19
 FT DISULFID 13 24
 FT MOD_RES 10 10 HYDROXYLATION.
 FT MOD_RES 11 11 HYDROXYLATION.
 SQ SEQUENCE 30 AA; 3186 MW; D9419BC6F0DB7A30 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RGK 13
 |||
 Db 21 RGK 23

RESULT 29

DMS3_PHYSA

ID DMS3_PHYSA STANDARD; PRT; 30 AA.
 AC P80279;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Dermaseptin 3 (DS III).
 OS Phyllomedusa sauvagei (Sauvage's leaf frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
 OC Phyllomedusinae; Phyllomedusa.
 OX NCBI_TaxID=8395;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=94139686; PubMed=8306981;
 RA Mor A., Nicolas P.;
 RT "Isolation and structure of novel defensive peptides from frog skin."
 RL Eur. J. Biochem. 219:145-154(1994).
 CC -!- FUNCTION: POSSESSES A POTENT ANTIMICROBIAL ACTIVITY AGAINST
 CC BACTERIA FUNGI AND PROTOZOA. PROBABLY ACTS BY DISTURBING MEMBRANE
 CC FUNCTIONS WITH ITS AMPHIPATIC STRUCTURE.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.
 CC Dermaseptin subfamily.
 KW Amphibian defense peptide; Antibiotic; Fungicide; Multigene family.
 SQ SEQUENCE 30 AA; 3024 MW; FD5F190C3DCBB0D7 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKL 28
 |||
 Db 23 KKL 25

RESULT 30

FTN_BACFR

ID FTN_BACFR STANDARD; PRT; 30 AA.
 AC P28733;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ferritin like protein (Fragment).
 OS Bacteroides fragilis.
 OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
 OC Bacteroidaceae; Bacteroides.
 OX NCBI_TaxID=817;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=20656-2-1;
 RX MEDLINE=92406001; PubMed=1526453;

RA Rocha E.R., Andrews S.C., Keen J.N., Brock J.H.;
 RT "Isolation of a ferritin from *Bacteroides fragilis*.";
 RL FEMS Microbiol. Lett. 74:207-212(1992).
 CC -!- FUNCTION: MAY ALLEVIATE IRON TOXICITY IN THE PRESENCE OF
 CC OXYGEN.
 CC -!- COFACTOR: BINDS ABOUT THREE IRON ATOMS PER MOLECULE.
 CC -!- SUBUNIT: FORMS OLIGOMERS OF ABOUT 400 kDa (THE MONOMER IS ABOUT
 CC 17 kDa).
 CC -!- SIMILARITY: BELONGS TO THE FERRITIN FAMILY. PROKARYOTIC SUBFAMILY.
 CC -!- SIMILARITY: Contains 1 ferritin-like diiron domain.
 DR InterPro; IPR001519; Ferritin.
 DR Pfam; PF00210; ferritin; 1.
 DR PROSITE; PS50905; FERRITIN_LIKE; 1.
 KW Iron storage; Iron; Metal-binding.
 FT DOMAIN 1 >30 FERRITIN-LIKE DIIRON.
 FT METAL 17 17 IRON (BY SIMILARITY).
 FT NON_TER 30 30
 SQ SEQUENCE 30 AA; 3529 MW; C70505B5696EFC4F CRC64;

 Query Match 8.8%; Score 3; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 27 KLQ 29
 |||
 Db 5 KLQ 7

RESULT 31

GLUM_ANGAN

ID GLUM_ANGAN STANDARD; PRT; 30 AA.
 AC P41521;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Glucagon-like peptide (GLP).
 OS *Anguilla anguilla* (European freshwater eel), and
 OS *Anguilla rostrata* (American eel).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;
 OC *Anguilla*.
 OX NCBI_TaxID=7936, 7938;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=*A.anguilla*, and *A.rostrata*;
 RC TISSUE=Pancreas;
 RX MEDLINE=91340068; PubMed=1874385;
 RA Conlon J.M., Andrews P.C., Thim L., Moon T.W.;
 RT "The primary structure of glucagon-like peptide but not insulin has
 RT been conserved between the American eel, *Anguilla rostrata* and the
 RT European eel, *Anguilla anguilla*.";
 RL Gen. Comp. Endocrinol. 82:23-32(1991).
 CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
 DR PIR; B61125; B61125.
 DR PIR; C61125; C61125.
 DR HSSP; P01275; 1BH0.
 DR InterPro; IPR000532; Glucagon.

DR Pfam; PF00123; hormone2; 1.
DR SMART; SM00070; GLUCA; 1.
DR PROSITE; PS00260; GLUCAGON; 1.
KW Glucagon family; Amidation.
FT MOD_RES 30 30 AMIDATION.
SQ SEQUENCE 30 AA; 3376 MW; 592DA5EABD6E49D0 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 LQD 30
|||
Db 14 LQD 16

RESULT 32

OTCC_AERPU

ID OTCC_AERPU STANDARD; PRT; 30 AA.
AC P11726;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ornithine carbamoyltransferase, catabolic (EC 2.1.3.3) (OTCase)
DE (Fragment).
OS Aeromonas punctata (Aeromonas caviae).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=648;
RN [1]
RP SEQUENCE.
RC STRAIN=NCIB 9232;
RX MEDLINE=85104799; PubMed=3968036;
RA Falmagne P., Portetelle D., Stalon V.;
RT "Immunological and structural relatedness of catabolic ornithine
RT carbamoyltransferases and the anabolic enzymes of enterobacteria."
RL J. Bacteriol. 161:714-719(1985).
CC -!- CATALYTIC ACTIVITY: Carbamoyl phosphate + L-ornithine = phosphate
CC + L-citrulline.
CC -!- PATHWAY: Arginine degradation via arginine deiminase; second step.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO THE ATCASES/OTCASES FAMILY.
DR InterPro; IPR006130; Asp/Orn_COtranf.
DR InterPro; IPR006132; OTCace_P.
DR Pfam; PF02729; OTCace_N; 1.
DR PROSITE; PS00097; CARBAMOYLTRANSFERASE; PARTIAL.
KW Transferase; Arginine metabolism.
FT NON_TER 30 30
SQ SEQUENCE 30 AA; 3654 MW; 673CB989FE72F9C1 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 EIQ 6
|||
Db 19 EIQ 21

RESULT 33

PCCA_MYXXA

ID PCCA_MYXXA STANDARD; PRT; 30 AA.
 AC P81185;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Propionyl-CoA carboxylase alpha chain (EC 6.4.1.3) (PCCASE)
 DE (Propanoyl-CoA:carbon dioxide ligase) (Fragment).
 OS Myxococcus xanthus.
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
 OC Cystobacterineae; Myxococcaceae; Myxococcus.
 OX NCBI_TaxID=34;
 RN [1]
 RP SEQUENCE, AND CHARACTERIZATION.
 RC STRAIN=ATCC 25232 / IFO 13542;
 RX MEDLINE=98350029; PubMed=9683657;
 RA Kimura Y., Kojyo T., Kimura I., Sato M.;
 RT "Propionyl-CoA carboxylase of Myxococcus xanthus: catalytic properties
 RT and function in developing cells."
 RL Arch. Microbiol. 170:179-184(1998).
 CC -!- FUNCTION: PROPIONYL-COA CARBOXYLASE ALSO CARBOXYLATES ACETYL-COA,
 CC BUTYRYL-COA AND SUCCINYL-COA BUT EXHIBITS DIFFERENT KM VALUES.
 CC -!- CATALYTIC ACTIVITY: ATP + propanoyl-CoA + HCO(3)(-) = ADP +
 CC phosphate + (S)-methylmalonyl-CoA.
 CC -!- COFACTOR: Biotin.
 CC -!- ENZYME REGULATION: By ATP and Mg(2+).
 CC -!- PATHWAY: KEY ENZYME IN THE CATABOLIC PATHWAY OF ODD-CHAIN
 CC FATTY ACIDS, ISOLEUCINE, THREONINE, METHIONINE, AND VALINE.
 CC -!- SUBUNIT: DODECAMER COMPOSED OF SIX BIOTIN-CONTAINING ALPHA
 CC SUBUNITS AND SIX BETA SUBUNITS (PROBABLE).
 CC -!- MISCELLANEOUS: IT SHOWS THE MAXIMAL ACTIVITY AT PH 7.0-7.5 AND AT
 CC TEMPERATURE OF 25-30 DEGREES CELSIUS.
 CC -!- MISCELLANEOUS: DURING DEVELOPMENT THE ACTIVITY INCREASED GRADUALLY
 CC WITH THE MAXIMUM DURING THE SPORULATION STAGE.
 DR HSSP; P24182; 1DV1.
 DR InterPro; IPR001882; Biotin_attach.
 DR InterPro; IPR005481; CPase_L_N.
 DR Pfam; PF00289; CPSase_L_chain; 1.
 DR PROSITE; PS00188; BIOTIN; PARTIAL.
 KW Ligase; Biotin; ATP-binding; Fatty acid biosynthesis.
 FT NON_TER 30 30
 SQ SEQUENCE 30 AA; 3343 MW; 05D3D2827BCDDD81 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NRG 12
 |||
 Db 10 NRG 12

RESULT 34

PCG2_PACGO

ID PCG2_PACGO STANDARD; PRT; 30 AA.
AC P82415;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ponericin G2.
OS Pachycondyla goeldii (Ponerine ant).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Formicidae;
OC Ponerinae; Pachycondyla.
OX NCBI_TaxID=118888;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=Venom;
RX MEDLINE=21264562; PubMed=11279030;
RA Orivel J., Redeker V., Le Caer J.-P., Krier F., Revol-Junelles A.-M.,
RA Longeon A., Chafotte A., Dejean A., Rossier J.;
RT "Ponericins, new antibacterial and insecticidal peptides from the
RT venom of the ant Pachycondyla goeldii.";
RL J. Biol. Chem. 276:17823-17829(2001).
CC -!- FUNCTION: BROAD SPECTRUM OF ACTIVITY AGAINST BOTH GRAM-POSITIVE
CC AND GRAM-NEGATIVE BACTERIA AND S.CEREVISIAE. HAS INSECTICIDAL
CC AND NON-HEMOLYTIC ACTIVITIES.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=3306.56; METHOD=MALDI.
KW Antibiotic; Insect immunity; Fungicide.
SQ SEQUENCE 30 AA; 3308 MW; A12CD4D0BAF40B5D CRC64;

Query Match 8.8%; Score 3; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 EWL 24
|||
Db 11 EWL 13

RESULT 35

PCG3_PACGO
ID PCG3_PACGO STANDARD; PRT; 30 AA.
AC P82416;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ponericin G3.
OS Pachycondyla goeldii (Ponerine ant).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Formicidae;
OC Ponerinae; Pachycondyla.
OX NCBI_TaxID=118888;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=Venom;
RX MEDLINE=21264562; PubMed=11279030;
RA Orivel J., Redeker V., Le Caer J.-P., Krier F., Revol-Junelles A.-M.,
RA Longeon A., Chafotte A., Dejean A., Rossier J.;
RT "Ponericins, new antibacterial and insecticidal peptides from the

RT venom of the ant *Pachycondyla goeldii*.
 RL J. Biol. Chem. 276:17823-17829(2001).
 CC -!- FUNCTION: BROAD SPECTRUM OF ACTIVITY AGAINST BOTH GRAM-POSITIVE
 CC AND GRAM-NEGATIVE BACTERIA AND *S.CEREVISIAE*. HAS INSECTICIDAL
 CC AND NON-HEMOLYTIC ACTIVITIES.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- MASS SPECTROMETRY: MW=3381.36; METHOD=MALDI.
 KW Antibiotic; Insect immunity; Fungicide.
 SQ SEQUENCE 30 AA; 3383 MW; BC0463D0AF140B53 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 EWL 24
 |||
 Db 11 EWL 13

RESULT 36

RKGG_LEPKE
 ID RKGG_LEPKE STANDARD; PRT; 30 AA.
 AC P21587;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 01-AUG-1991 (Rel. 19, Last annotation update)
 DE Rathke's gland glycoprotein (Fragment).
 OS *Lepidochelys kemp*i (Atlantic ridley) (Kemp's ridley sea turtle).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Testudines; Cryptodira; Chelonioidea; Cheloniidae; *Lepidochelys*.
 OX NCBI_TaxID=8472;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Rathke's gland;
 RX MEDLINE=90075703; PubMed=2591198;
 RA Radhakrishna G., Chin C.C.Q., Wold F., Weldon P.J.;
 RT "Glycoproteins in Rathke's gland secretions of loggerhead (*Caretta*
 RT *caretta*) and Kemp's ridley (*Lepidochelys kemp*i) sea turtles."
 RL Comp. Biochem. Physiol. 94B:375-378(1989).
 CC -!- FUNCTION: RATHKE'S GLAND SECRETIONS MAY FUNCTION AS PHEROMONES,
 CC AS PREDATOR REPELLANTS, OR CONTRIBUTE TO THE MAINTENANCE OF THE
 CC TURTLE SHELL.
 CC -!- SIMILARITY: WITH RATHKE'S GLAND GLYCOPROTEIN FROM LOGGERHEAD SEA
 CC TURTLE.
 DR PIR; PL0155; PL0155.
 KW Glycoprotein.
 FT NON_TER 30 30
 SQ SEQUENCE 30 AA; 3019 MW; F5DF5F80F582ED84 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RGK 13
 |||
 Db 16 RGK 18

RESULT 37

TX2_THRPR

ID TX2_THRPR STANDARD; PRT; 30 AA.
 AC P83476;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Toxin ProTx-II.
 OS Thrixopelma pruriens (Green velvet).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
 OC Mygalomorphae; Theraphosidae; Thrixopelma.
 OX NCBI_TaxID=213387;
 RN [1]
 RP SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, MASS
 RP SPECTROMETRY, AND DISULFIDE BONDS.
 RC TISSUE=Venom;
 RX MEDLINE=22363233; PubMed=12475222;
 RA Middleton R.E., Warren V.A., Kraus R.L., Hwang J.C., Liu C.J., Dai G.,
 RA Brochu R.M., Kohler M.G., Gao Y.-D., Garsky V.M., Bogusky M.J.,
 RA Mehl J.T., Cohen C.J., Smith M.M.;
 RT "Two tarantula peptides inhibit activation of multiple sodium
 RT channels.";
 RL Biochemistry 41:14734-14747(2002).
 CC -!- FUNCTION: Inhibits voltage-gated calcium and sodium channels.
 CC Shifts the voltage-dependence of channel activation to more
 CC positive potentials.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
 CC -!- MASS SPECTROMETRY: MW=3827; METHOD=Electrospray.
 CC -!- MASS SPECTROMETRY: MW=3827; METHOD=MALDI.
 CC -!- SIMILARITY: BELONGS TO THE SPIDER POTASSIUM CHANNEL INHIBITORY
 CC TOXIN FAMILY.
 KW Toxin; Neurotoxin; Ionic channel inhibitor; Calcium channel inhibitor;
 KW Sodium channel inhibitor.
 FT DISULFID 2 16
 FT DISULFID 9 21
 FT DISULFID 15 25
 SQ SEQUENCE 30 AA; 3833 MW; 5B8CF4C6338C1B9B CRC64;

Query Match 8.8%; Score 3; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKL 28
 |||
 Db 27 KKL 29

RESULT 38

UP61_UPEIN

ID UP61_UPEIN STANDARD; PRT; 30 AA.
 AC P82037;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Uperin 6.1.

OS Uperoleia inundata (Floodplain toadlet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
 OC Myobatrachinae; Uperoleia.
 OX NCBI_TaxID=104953;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RA Bradford A.M., Raftery M.J., Bowie J.H., Tyler M.J., Wallace J.C.,
 RA Adams G.W., Severini C.;
 RT "Novel uperin peptides from the dorsal glands of the australian
 RT floodplain toadlet Uperoleia inundata.";
 RL Aust. J. Chem. 49:475-484(1996).
 CC -!- FUNCTION: UNKNOWN.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
 CC -!- MASS SPECTROMETRY: MW=3233.85; METHOD=MALDI.
 KW Amphibian defense peptide.
 SQ SEQUENCE 30 AA; 3233 MW; 4EE15B9EB110F68E CRC64;

Query Match 8.8%; Score 3; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 KKL 28
 |||
 Db 24 KKL 26

RESULT 39

UP62_UPEIN

ID UP62_UPEIN STANDARD; PRT; 30 AA.
 AC P82038;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Uperin 6.2.
 OS Uperoleia inundata (Floodplain toadlet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
 OC Myobatrachinae; Uperoleia.
 OX NCBI_TaxID=104953;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RA Bradford A.M., Raftery M.J., Bowie J.H., Tyler M.J., Wallace J.C.,
 RA Adams G.W., Severini C.;
 RT "Novel uperin peptides from the dorsal glands of the australian
 RT floodplain toadlet Uperoleia inundata.";
 RL Aust. J. Chem. 49:475-484(1996).
 CC -!- FUNCTION: UNKNOWN.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
 CC -!- MASS SPECTROMETRY: MW=3261.85; METHOD=MALDI.
 KW Amphibian defense peptide.
 SQ SEQUENCE 30 AA; 3261 MW; 4EE15B9EB10841DE CRC64;

Query Match 8.8%; Score 3; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKL 28
|||
Db 24 KKL 26

RESULT 40

VAA2_EQUAR

ID VAA2_EQUAR STANDARD; PRT; 30 AA.
AC Q04238;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Vacuolar ATP synthase catalytic subunit A, isoform 2 (EC 3.6.3.14)
DE (Fragment).
OS Equisetum arvense (Field horsetail) (Common horsetail).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Equisetophyta; Sphenopsida; Equisetales; Equisetaceae; Equisetum.
OX NCBI_TaxID=3258;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93138084; PubMed=8422915;
RA Starke T., Gogarten J.P.;
RT "A conserved intron in the V-ATPase A subunit genes of plants and
RT algae.";
RL FEBS Lett. 315:252-258(1993).
CC -!- FUNCTION: CATALYTIC SUBUNIT OF THE PERIPHERAL V1 COMPLEX OF
CC VACUOLAR ATPASE. V-ATPASE VACUOLAR ATPASE IS RESPONSIBLE FOR
CC ACIDIFYING A VARIETY OF INTRACELLULAR COMPARTMENTS IN EUKARYOTIC
CC CELLS.
CC -!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) = ADP + phosphate +
CC H(+) (Out).
CC -!- SUBUNIT: V-ATPASE IS AN HETEROMULTIMERIC ENZYME COMPOSED OF A
CC PERIPHERAL CATALYTIC V1 COMPLEX (MAIN COMPONENTS: SUBUNITS A, B,
CC C, D, E, AND F) ATTACHED TO AN INTEGRAL MEMBRANE V0 PROTON PORE
CC COMPLEX (MAIN COMPONENT: THE PROTEOLIPID PROTEIN).
CC -!- MISCELLANEOUS: TWO SEPARATE GENES ENCODE THE CATALYTIC 70 kDa
CC V-ATPASE SUBUNIT IN PSILOTUM AND EQUISETUM.
CC -!- SIMILARITY: Belongs to the ATPase alpha/beta chains family.

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DR EMBL; X56984; CAA40302.1; -.
DR PIR; S21815; S21815.
DR InterPro; IPR000194; ATPase_a/bcentre.
DR PROSITE; PS00152; ATPASE_ALPHA_BETA; PARTIAL.
KW ATP synthesis; Hydrogen ion transport; Hydrolase; ATP-binding;
KW Multigene family.

FT NON_TER 1 1
FT NON_TER 30 30
SQ SEQUENCE 30 AA; 3372 MW; 51CCA4A3DA9E5D84 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 MER 20
|||
Db 23 MER 25

Search completed: January 14, 2004, 10:35:31
Job time : 6.61371 secs